

tgccttcatt cccaggagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggtcttt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctcctaacga ggaaatcacc tgggggtgtct atgaatggac tagatttgcc tcagtgggtt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 ccttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggg gacgatatcg tatag 2565

<210> 39  
 <211> 2565  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg1\_will\_amplicon\_cds\_2

<400> 39

atggtagtag cagtggagaa aaccaacctc acttcacaat cacaatgctt caaccgtgtt 60  
 tctgacaaga agaaagaaag atgcaagaca cacatgaaca acgttaaccc atgttgtttt 120  
 ttgtttctct tatgtgtgtg gagccttggt gtgctccctt catgcgtgag gccagttttg 180  
 tgtgaagatg aaggttggga tggagtgggt gtgacagcat caaacctctt agcacttgaa 240  
 gctttcaagc aagagttggt tgatccagaa gggttcttgc ggagctggaa tgacagtggc 300  
 tatggagctt gttccggagg ttgggttggga atcaagtgtg ctaagggaca ggttattgtg 360  
 atccagcttc cttggaaggg tttgaggggt cgaatcaccg acaaaattgg tcaacttcaa 420  
 ggcttcagga agcttagtct tcatgataac caaattgggt gttcaatccc ttcaactttg 480  
 ggacttcttc ccaaccttag aggggttcag ttattcaaca ataggcttac aggttccata 540  
 cctctttctt taggtttctg ccctttgctt cagtctcttg acctcagcaa caacttgctc 600  
 acaggagcaa tcccttatag tcttgctaat tccactaagc tttattggct taacttgagt 660  
 ttcaactcct tctctggtec tttaccagct agcctaactc actcattttc tctcactttt 720  
 ctttctcttc aaaataacaa tctttctggc tcccttccta actcttgggg tgggaattcc 780  
 aagaatggct tctttaggct tcaaaatttg atcctagatc ataacttttt cactgggtgac 840  
 gttcctgctt ctttgggtag cttaagagag ctcaatgaga tttcccttag tcataataag 900

tttagtggag ctataccaaa tgaaatagga accctttcta ggcttaagac acttgacatt 960  
 tctaataatg ccttgaatgg gaacttgcct gctaccctat ctaatttatc ctcaacttaca 1020  
 ctgctgaatg cagagaacaa cctccttgac aatcaaattc ctcaaagttt aggttagattg 1080  
 cgtaatcttt ctgttctgat tttgagtaga aaccaattta gtggacatat tccttcaagt 1140  
 attgcaaaca tttcctcgct taggcagctt gatttgtcac tgaataattt cagtggagaa 1200  
 attccagctt cctttgacag tcagcgcagt ctaaattctt tcaatgtttc ctacaatagc 1260  
 ctctcagggt ctgtccccc tctgcttgcc aagaaattta actcaagctc atttgtggga 1320  
 aatattcaac tatgtggata cagcccttca accccatgtc tttcccaagc tccatcacia 1380  
 ggagtcattg ccccacctcc tgaagtgtca aaacatcacc atcataggaa gctaagcacc 1440  
 aaagacataa ttctcatagt agcaggagtt ctccctcgtag tcctgattat actttgttgt 1500  
 gtccctgctt tctgcctgat cagaaagaga tcaacatcta aggccgggaa cggccaagcc 1560  
 accgagggta gagcggccac tatgaggaca gaaaaaggag tccctccagt tgctgggtgt 1620  
 gatgttgaag caggtgggga ggctggaggg aaactagtcc attttgatgg accaatggct 1680  
 tttacagctg atgatctctt gtgtgcaaca gctgagatca tgggaaagag cacctatgga 1740  
 actgtttata aggctatttt ggaggatgga agtcaagttg cagtaaagag attgagggaa 1800  
 aagatcacta aaggtcatag agaatttgaa tcagaagtca gtgttctagg aaaaattaga 1860  
 caccccaatg ttttggtctt gagagcctat tacttgggac ccaaagggga aaagcttctg 1920  
 gtttttgatt acatgtctaa aggaagtctt gcttctttcc tacatggtgg tggaactgaa 1980  
 acattcattg attggccaac aagaatgaaa atagcacaag acttggccccg tggcttggtc 2040  
 tgccttcatt ccaggagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggtcttt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctccaaacga ggaaatcacc tggggtgtct atgaatggac tagatttgcc tcagtgggtt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 ctttctccat cagcacgacc agaagttcat caagtctctc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggt gacgatatcg tatag 2565

<210> 40  
 <211> 2565  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg1\_a2704\_amplicon\_cds\_2

<400> 40

```

atggtagtag cagtggagaa aaccaacctc acttcacaat cacaatgctt caaccgtggt 60
tctgacaaga agaaagaaag atgcaagaca cacatgaaca acgttaaccc atgttggttt 120
ttgtttctct tatgtgtgtg gagccttggt gtgctcccct catgcgtgag gccagttttg 180
tgtgaagatg aagggttgga tggagtgggt gtgacagcat caaacctctt agcacttgaa 240
gctttcaagc aagagtttgt tgatccagaa gggttcttgc ggagctggaa tgacagtggc 300
tatggagctt gtcccgagg ttgggttgga atcaagtgtg ctaagggaca gggtattgtg 360
atccagcttc cttggaaggg tttaggggt cgaatcaccg acaaaattgg tcaacttcaa 420
ggcctcagga agcttagtct tcatgataac caaattgggt gttcaatccc ttcaactttg 480
ggacttcttc ccaaccttag aggggttcag ttattcaaca ataggcttac aggttcata 540
cctctttctt taggtttctg ccctttgctt cagtctcttg acctcagcaa caacttgctc 600
acaggagcaa tcccttatag tcttgcta atccactaagc tttattggct taacttgagt 660
ttcaactcct tctctggtcc tttaccagct agcctaactc actcattttc tctcactttt 720
ctttctcttc aaaataacaa tctttctggc tcccttccta actcttgggg tgggaattcc 780
aagaatggct tctttaggct tcaaaatttg atcctagatc ataacttttt cactggtgac 840
gttcctgctt ctttgggtag cttaagagag ctcaatgaga tttcccttag tcataataag 900
tttagtggag ctataccaaa tgaaatagga accctttcta ggcttaagac acttgacatt 960
tctaataatg ccttgaatgg gaacttgctt gctaccctat ctaatttatc ctacttaca 1020
ctgctgaatg cagagaacaa cctccttgac aatcaaattc ctcaaagttt aggtagattg 1080
cgtaatcttt ctgttctgat tttagagtag aaccaattta gtggacatat tcttcaagt 1140
attgcaaaca tttctcgct taggcagctt gatttgtcac tgaataattt cagtggagaa 1200
attccagtct ccttcgacag tcagcgcagt ctaaattctt tcaatgtttc ctacaatagc 1260
ctttcagggt ctgttcccc tctgcttgcc aagaaattta actcaagctc atttgtggga 1320
aatattcaac tatgtgggta cagcccttca accccatgtc tttcccaagc tccatcaca 1380
ggagtcattg cccacctcc tgaagtgtca aaacatcacc atcataggaa gctaagcacc 1440

```

aaagacataa ttctcatagt agcaggagtt ctctctgtag ttctgattat actttgttgt 1500  
 gtctgtcttt tctgcctgat cagaaagaga tcaacatcta aggccgggaa cggccaagcc 1560  
 accgagggta gagcggccac tatgaggaca gaaaaaggag tccctccagt tgctgctggt 1620  
 gatgttgaag caggtgggga ggctggaggg aaactagtcc attttgatgg accaatggct 1680  
 ttacagctg atgatctctt gtgtgcaaca gctgagatca tgggaaagag cacctatgga 1740  
 actgtttata aggctatttt ggaggatgga agtcaagttg cagtaaagag attgagggaa 1800  
 aagatcacta aaggctcatag agaatttgaa tcagaagtca gtgttctagg aaaaattaga 1860  
 caccccaatg ttttggctct gagggcctat tacttgggac ccaaagggga aaagcttctg 1920  
 gtttttgatt acatgtctaa aggaagtctt gcttctttcc tacatggtgg tggaactgaa 1980  
 acattcattg attggccaac aaggatgaaa atagcacaag acttggcccg tggcttggtc 2040  
 tgccttcatt cccaggagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggtcttt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctctaacga ggaaatcacc tggggtgcct atgaatggac tagatttgcc tcagtggggt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 ccttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggg gacgatatcg tatag 2565

<210> 41  
 <211> 2565  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg1\_noir\_amplicon\_cds\_2

<400> 41

atggtagtag cagtggagaa aaccaacctc acttcacaat cacaatgctt caaccgtgtt 60  
 tctgacaaga agaaagaaag atgcaagaca cacatgaaca acgttaacct atgttgtttt 120  
 ttgtttctct tatgtgtgtg gagccttggt gtgctccct catgcgtgag gccagttttg 180  
 tgtgaagatg aaggttggga tggagtgggt gtgacagcat caaacctctt agcacttgaa 240  
 gctttcaagc aagagttggt tgatccagaa gggttcttgc ggagctggaa tgacagtggc 300



tatggagctt gttccggagg ttgggttga atcaagtgtg ctcagggaca ggttattgtg 360  
 atccagcttc cttggaaggg tttgaggggt cgaatcaccg acaaaattgg ccaacttcaa 420  
 ggcctcagga agcttagtct tcatgataac caaattggtg gttcaatccc ttcaactttg 480  
 ggacttcttc ccaaccttag aggggttcag ttattcaaca ataggcttac aggttccata 540  
 cctctttctt taggtttctg ccttttgctt cagtctcttg acctcagcaa caacttgctc 600  
 acaggagcaa tcccttatag tcttgctaata tccactaagc tttattggct taacttgagt 660  
 ttcaactcct tctctggtcc tttaccagct agcctaactc actcattttc tctcactttt 720  
 ctttctcttc aaaataacaa tctttctggc tcccttccta actcttgggg tggaaattcc 780  
 aagaatggct tcttttaggt tcaaaatttg atcctagata ataacttttt cactggtgac 840  
 gttcctgctt ctttgggtag cttaagagag ctcaatgaga tttcccttag tcataataag 900  
 tttagtggag ctataccaaa tgaaatagga accctttcta ggcttaagac acttgacatt 960  
 tctaataatg ccttgaatgg gaacttgcct gctaccctct ctaatttatc ctcacttaca 1020  
 ctgctgaatg cagagaacaa cctccttgac aatcaaatcc ctcaaagttt aggtagattg 1080  
 cgtaatcttt ctgttctgat tttgagtaga aaccaattta gtggacatat tccctcaagc 1140  
 attgcaaaca tttcctcgct taggcagctt gatttgtcac tgaataattt cagtggagaa 1200  
 attccagctc ccttcgacag tcagcgcagt ctaaactctt tcaatgtttc ctacaatagc 1260  
 ctttcagggt ctgttcccc tctgcttgcc aagaaattta actcaagctc atttggtgga 1320  
 aatattcaac tatgtgggta cagcccttca acccatgtc tttcccaagc tccatcacia 1380  
 ggagtcattg cccacctcc tgaagtgtca aaacatcacc atcataggaa gctaagcacc 1440  
 aaagacataa ttctcatagt agcaggagtt ctctcgtag ttctgattat actttgttgt 1500  
 gtcttgcttt tctgcctgat cagaaagaga tcaacatcta aggccgggaa cggccaagcc 1560  
 accgagggta gagcggccac tatgaggaca gaaaaaggag tccctccagt tgctgctggt 1620  
 gatgttgaag caggtgggga ggctggaggg aaactagtcc attttgatgg accaatggct 1680  
 tttacagctg atgatctctt gtgtgcaaca gctgagatca tgggaaagag cacctatgga 1740  
 actgtttata aggctatttt ggaggatgga agtcaagttg cagtaaagag attgagggaa 1800  
 aagatcacta aaggctatag agaatttgaa tcagaagtca gtgttctagg aaaaattaga 1860  
 caccccaatg ttttggctct gagggcctat tacttgggac ccaaagggga aaagcttctg 1920  
 gtttttgatt acatgtctaa aggaagtctt gcttctttcc tacatggtgg tggaactgaa 1980  
 acattcattg attggccaac aaggatgaaa atagcacaag acttggcccc tggcttgctc 2040

tgccttcatt cccaggagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggctctt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctctaacga ggaaatcacc tgggggtgcct atgaatggac tagatttgcc tcagtgggtt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 ccttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggt gacgatatcg tatag 2565

<210> 42  
 <211> 2565  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg1\_lee\_amplicon\_cds\_2

<400> 42

atggtagtag cagtggagaa aaccaacctc acttcacaat cacaatgctt caaccgtgtt 60  
 tctgacaaga agaaagaaag atgcaagaca cacatgaaca acgttaaccc atgttggttt 120  
 ttgtttctct tatgtgtgtg gagccttggt gtgctccct catgcgtgag gccagttttg 180  
 tgtgaagatg aagggtggga tggagtgggt gtgacagcat caaacctctt agcacttgaa 240  
 gctttcaagc aagagtgggt tgatccagaa gggttcttgc ggagctggaa tgacagtggc 300  
 tatggagctt gttccggagg ttgggttgga atcaagtgtg ctcagggaca ggttattgtg 360  
 atccagcttc cttggaaggg tttgaggggt cgaatcaccc aaaaattgg ccaacttcaa 420  
 ggccctcagga agcttagtct tcatgataac caaattgggt gttcaatccc ttcaactttg 480  
 ggacttcttc ccaaccttag aggggttcag ttattcaaca ataggcttac aggttccata 540  
 cctctttctt taggtttctg ccctttgctt cagtctcttg acctcagcaa caacttgctc 600  
 acaggagcaa tcccttatag tcttgctaatt tccactaagc tttattggct taacttgagt 660  
 ttcaactcct tctctgggtc tttaccagct agcctaactc actcattttc tctcactttt 720  
 ctttctcttc aaaataacaa tctttctggc tcccttccta actcttgggg tgggaattcc 780  
 aagaatggct tctttaggct tcaaaatttg atcctagata ataacttttt cactgggtgac 840  
 gttcctgctt ctttgggtag ctttaagagag ctcaatgaga tttcccttag tcataataag 900

tttagtggag ctataccaaa tgaaatagga acccttttcta ggcttaagac acttgacatt 960  
 tctaataatg ccttgaatgg gaacttgcct gctaccctct ctaatttatc ctcacttaca 1020  
 ctgctgaatg cagagaacaa cctccttgac aatcaaatacc ctcaaagttt aggtagattg 1080  
 cgtaatcttt ctgttctgat tttgagtaga aaccaattta gtggacatat tccttcaagc 1140  
 attgcaaaca tttcctcgct taggcagctt gatttgtcac tgaataattt cagtggagaa 1200  
 attccagtct ccttcgacag tcagcgcagt ctaaactctt tcaatgtttc ctacaatagc 1260  
 ctttcagggt ctgttcccc tctgcttgcc aagaaattta actcaagctc atttgtggga 1320  
 aatattcaac tatgtgggta cagcccttca acccatgtc tttccaagc tccatcacia 1380  
 ggagtcattg cccacctcc tgaagtgtca aaacatcacc atcataggaa gctaagcacc 1440  
 aaagacataa ttctcatagt agcaggagtt ctctctgtag ttctgattat actttgttgt 1500  
 gtcttgcttt tctgcctgat cagaaagaga tcaacatcta aggccgggaa cggccaagcc 1560  
 accgagggtg gagcgccac tatgaggaca gaaaaggag tccctccagt tgctgctggt 1620  
 gatgttgaag caggtgggga ggctggagg aaactagtcc attttgatgg accaatggct 1680  
 tttacagctg atgatctctt gtgtgcaaca gctgagatca tgggaaagag cacctatgga 1740  
 actgtttata aggtatttt ggaggatgga agtcaagttg cagtaaagag attgaggga 1800  
 aagatcacta aaggtcatag agaatttgaa tcagaagtca gtgttctagg aaaaattaga 1860  
 caccccaatg ttttggctct gagggcctat tacttgggac ccaaaggga aaagcttctg 1920  
 gtttttgatt acatgtctaa aggaagtctt gcttctttcc tacatggtgg tggaaactgaa 1980  
 acattcattg attggccaac aaggatgaaa atagcacaag acttggcccg tggcttggtc 2040  
 tgccttcatt ccagagagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggtcttt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctctaacga ggaaatcacc tgggtgcct atgaatggac tagatttgcc tcagtgggtt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 cttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggt gacgatatcg tatag 2565

<210> 43  
 <211> 2565  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg1\_pi200499\_amplicon\_cds\_2

<400> 43

```

atggtagtag cagtggagaa aaccaacctc acttcacaat cacaatgctt caaccgtgtt   60
tctgacaaga agaaagaaag atgcaagaca cacatgaaca acgttaaccc atgttgtttt  120
ttgtttctct tatgtgtgtg gagccttggt gtgctcccct catgctgtgag gccagttttg  180
tgtgaagatg aaggttggga tggagtgggt gtgacagcat caaacctctt agcacttgaa  240
gctttcaagc aagagtgggt tgatccagaa gggttcttgc ggagctggaa tgacagtggc  300
tatggagctt gttccggagg ttgggttggga atcaagtgtg ctcagggaca ggttattgtg  360
atccagcttc cttggaaggg ttgaggggt cgaatcaccc acaaaattgg ccaacttcaa  420
ggcctcagga agcttagtct tcatgataac caaattgggt gttcaatccc ttcaactttg  480
ggactttctt ccaaccttag aggggttcag ttattcaaca ataggcttac aggttccata  540
cctctttctt taggtttctg ccctttgctt cagtctcttg acctcagcaa caacttgctc  600
acaggagcaa tcccttatag tcttgcta atccactaagc tttattggct taacttgagt  660
ttcaactcct tctctggtcc tttaccagct agcctaactc actcattttc tctcactttt  720
ctttctcttc aaaataacaa tctttctggc tcccttccta actcttgggg tgggaattcc  780
aagaatggct tctttaggct tcaaaatttg atcctagata ataacttttt cactggtgac  840
gttctgtgct ctttgggtag cttaagagag ctcaatgaga tttcccttag tcataataag  900
tttagtggag ctataccaaa tgaaatagga accctttcta ggcttaagac acttgacatt  960
tctaataatg ccttgaatgg gaacttgcct gctaccctct ctaattttat ctcacttaca 1020
ctgctgaatg cagagaacaa cctccttgac aatcaaatac ctcaaagttt aggtagattg 1080
cgtaatcttt ctgttctgat tttgagtaga aaccaattta gtggacatat tcttcaagc 1140
attgcaaaca tttcctcgct taggcagctt gatttgtcac tgaataattt cagtggagaa 1200
attccagctc ccttcgacag tcagcgcagt ctaaattctt tcaatgtttc ctacaatagc 1260
ctttcaggtt ctgttcccc tctgcttgcc aagaaattta actcaagctc atttgtggga 1320
aatattcaac tatgtgggta cagcccttca acccatgtc tttccaagc tccatcacia 1380
ggagtcaattg cccacctcc tgaagtgtca aaacatcacc atcataggaa gctaagcacc 1440
aaagacataa ttctcatagt agcaggagtt ctctcgtag ttctgattat actttgttgt 1500

```

gtctctgcttt tctgcctgat cagaaagaga tcaacatcta aggccgggaa cggccaagcc 1560  
 accgagggtta gagcggccac tatgaggaca gaaaaaggag tccctccagt tgctgctggt 1620  
 gatgttgaag caggtgggga ggctggaggg aaactagtcc attttgatgg accaatggct 1680  
 ttacagctg atgatctctt gtgtgcaaca gctgagatca tgggaaagag cacctatgga 1740  
 actgtttata aggctatfff ggaggatgga agtcaagttg cagtaaagag attgagggaa 1800  
 aagatcacta aaggatcatag agaatttgaa tcagaagtca gtgttctagg aaaaattaga 1860  
 caccccaatg ttttggctct gagggcctat tacttgggac ccaaagggga aaagcttctg 1920  
 gtttttgatt acatgtctaa aggaagtctt gcttctttcc tacatggtgg tggaaactgaa 1980  
 acattcattg attggccaac aaggatgaaa atagcacaag acttggcccg tggcttggtc 2040  
 tgcttcatt cccaggagaa catcatacat gggaacctca catccagcaa tgtgttgctt 2100  
 gatgagaata caaatgctaa aattgcagat tttggctctt ctcggttgat gtcaactgct 2160  
 gctaattcca acgtgatagc tacagctgga gcattgggat accgggcacc tgagctctca 2220  
 aagctcaaga aagcaaacac taaaactgat atctacagtc ttggtgttat cttgttagaa 2280  
 ctcttaacga ggaaatcacc tgggggtgcct atgaatggac tagatttgcc tcagtgggtt 2340  
 gcctcagttg tcaaagagga gtggacaaat gaggtttttg atgcagactt gatgagagat 2400  
 gcatccacag ttggcgacga gttgctaaac acgttgaagc tcgctttgca ctgtgttgat 2460  
 cttctccat cagcacgacc agaagttcat caagttctcc agcagctgga agagattaga 2520  
 ccagagagat cagtcacagc cagtcccggg gacgatatcg tatag 2565

<210> 44  
 <211> 3480  
 <212> DNA  
 <213> Glycine max  
  
 <220>  
 <221> CDS  
 <222> (79)..(2242), (2958)..(3478)  
  
 <223> Seq ID: rhg4\_a3244\_amplicon  
  
 <400> 44

atgtctctcc ccaaaaccct actttctctc ttcttctcc tcacgatccc cctagtaacc 60  
  
 gccgatgacg ccgcggtg atg tcg aat ttt ctc aaa tcc ctc act cca ccg 111  
                   Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro  
                   1                  5                  10  
  
 ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc 159

|     |     |     |     |     |        |     |     |     |     |     |     |        |     |     |     |     |
|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|
| Pro | Ser | Gly | Trp | Ser | Glu    | Thr | Thr | Pro | Phe | Cys | Gln | Trp    | Lys | Gly | Ile |     |
|     |     | 15  |     |     |        |     |     | 20  |     |     |     |        | 25  |     |     |     |
| caa | tgc | gat | tca | tcc | agc    | cac | gtg | acc | agc | ata | agc | ctc    | gct | tcg | cat | 207 |
| Gln | Cys | Asp | Ser | Ser | Ser    | His | Val | Thr | Ser | Ile | Ser | Leu    | Ala | Ser | His |     |
|     |     | 30  |     |     |        |     | 35  |     |     |     | 40  |        |     |     |     |     |
| tcc | ctc | acc | gga | aca | ctc    | ccc | tcg | gat | ctc | aat | tcc | ctc    | tct | caa | ctc | 255 |
| Ser | Leu | Thr | Gly | Thr | Leu    | Pro | Ser | Asp | Leu | Asn | Ser | Leu    | Ser | Gln | Leu |     |
|     |     | 45  |     |     |        | 50  |     |     |     | 55  |     |        |     |     |     |     |
| cgc | act | ctc | tcc | ctc | caa    | gac | aat | tcc | ctc | acc | ggc | acc    | ctc | cct | tct | 303 |
| Arg | Thr | Leu | Ser | Leu | Gln    | Asp | Asn | Ser | Leu | Thr | Gly | Thr    | Leu | Pro | Ser |     |
| 60  |     |     |     |     | 65     |     |     |     | 70  |     |     |        |     | 75  |     |     |
| ctc | tcc | aac | ctt | tct | ttc    | ctc | caa | acc | gtc | tac | tta | aac    | cgc | aac | aac | 351 |
| Leu | Ser | Asn | Leu | Ser | Phe    | Leu | Gln | Thr | Val | Tyr | Leu | Asn    | Arg | Asn | Asn |     |
|     |     |     | 80  |     |        |     |     | 85  |     |     |     | 90     |     |     |     |     |
| ttc | tcc | tcc | gtg | tcc | ccc    | acc | gct | ttc | gcc | tcc | cta | acc    | tcc | ctc | caa | 399 |
| Phe | Ser | Ser | Val | Ser | Pro    | Thr | Ala | Phe | Ala | Ser | Leu | Thr    | Ser | Leu | Gln |     |
|     |     |     | 95  |     |        |     | 100 |     |     |     |     | 105    |     |     |     |     |
| acc | ctc | agc | ctc | ggc | tcc    | aac | cct | gct | ctc | caa | ccc | tggtcc | ttc | ccc |     | 447 |
| Thr | Leu | Ser | Leu | Gly | Ser    | Asn | Pro | Ala | Leu | Gln | Pro | Trp    | Ser | Phe | Pro |     |
|     |     | 110 |     |     |        | 115 |     |     |     | 120 |     |        |     |     |     |     |
| acc | gac | ctc | act | tcc | tcc    | tct | aac | cta | atc | gac | ctc | gac    | ctc | gcc | acc | 495 |
| Thr | Asp | Leu | Thr | Ser | Ser    | Ser | Asn | Leu | Ile | Asp | Leu | Asp    | Leu | Ala | Thr |     |
|     |     | 125 |     |     |        | 130 |     |     |     | 135 |     |        |     |     |     |     |
| gta | tcc | ctc | acc | ggt | ccc    | ttg | ccg | gac | att | ttc | gac | aaa    | ttc | cct | tcc | 543 |
| Val | Ser | Leu | Thr | Gly | Pro    | Leu | Pro | Asp | Ile | Phe | Asp | Lys    | Phe | Pro | Ser |     |
| 140 |     |     |     |     | 145    |     |     |     | 150 |     |     |        |     | 155 |     |     |
| ctt | caa | cac | ctt | cgc | ctc    | tct | tac | aac | aac | ctc | acc | ggc    | aat | tta | ccc | 591 |
| Leu | Gln | His | Leu | Arg | Leu    | Ser | Tyr | Asn | Asn | Leu | Thr | Gly    | Asn | Leu | Pro |     |
|     |     |     | 160 |     |        |     |     | 165 |     |     |     | 170    |     |     |     |     |
| tcc | tct | ttc | tcc | gcc | gcc    | aac | aat | ctc | gaa | acg | ctc | tggtcc | ctc | aac | aac | 639 |
| Ser | Ser | Phe | Ser | Ala | Ala    | Asn | Asn | Leu | Glu | Thr | Leu | Trp    | Leu | Asn | Asn |     |
|     |     |     | 175 |     |        |     | 180 |     |     |     |     | 185    |     |     |     |     |
| cag | gcc | gcc | ggc | ttg | tcc    | ggt | acc | ctc | ctc | gtc | ctc | tcc    | aac | atg | tct | 687 |
| Gln | Ala | Ala | Gly | Leu | Ser    | Gly | Thr | Leu | Leu | Val | Leu | Ser    | Asn | Met | Ser |     |
|     |     | 190 |     |     |        | 195 |     |     |     | 200 |     |        |     |     |     |     |
| gca | tta | aac | cag | tcc | tggtcc | ctc | aat | aag | aac | cag | ttc | acc    | ggt | tcc | ata | 735 |
| Ala | Leu | Asn | Gln | Ser | Trp    | Leu | Asn | Lys | Asn | Gln | Phe | Thr    | Gly | Ser | Ile |     |
|     |     | 205 |     |     |        | 210 |     |     |     | 215 |     |        |     |     |     |     |
| ccg | gat | tta | tcg | caa | tgc    | acg | gct | ttg | tct | gac | ttg | cag    | ctc | agg | gat | 783 |
| Pro | Asp | Leu | Ser | Gln | Cys    | Thr | Ala | Leu | Ser | Asp | Leu | Gln    | Leu | Arg | Asp |     |
| 220 |     |     |     |     | 225    |     |     |     | 230 |     |     |        |     | 235 |     |     |
| aac | cag | tta | act | ggt | gtg    | gtt | ccc | gct | tca | ttg | aca | agt    | ctt | cct | agt | 831 |
| Asn | Gln | Leu | Thr | Gly | Val    | Val | Pro | Ala | Ser | Leu | Thr | Ser    | Leu | Pro | Ser |     |
|     |     |     | 240 |     |        |     |     | 245 |     |     |     |        | 250 |     |     |     |

|   |      |
|---|------|
| ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc | 879  |
| Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro |      |
| 255 260 265   |      |
| gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt | 927  |
| Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe |      |
| 270 275 280   |      |
| tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg | 975  |
| Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu |      |
| 285 290 295   |      |
| cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg | 1023 |
| Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp |      |
| 300 305 310 315   |      |
| aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc | 1071 |
| Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala |      |
| 320 325 330   |      |
| gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc | 1119 |
| Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr |      |
| 335 340 345   |      |
| atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc | 1167 |
| Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu |      |
| 350 355 360   |      |
| aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg | 1215 |
| Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu |      |
| 365 370 375   |      |
| cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg | 1263 |
| Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu |      |
| 380 385 390 395   |      |
| gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct | 1311 |
| Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala |      |
| 400 405 410   |      |
| ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act | 1359 |
| Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr |      |
| 415 420 425   |      |
| cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt | 1407 |
| Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly |      |
| 430 435 440   |      |
| aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg | 1455 |
| Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val |      |
| 445 450 455   |      |
| ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc | 1503 |
| Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val |      |
| 460 465 470 475   |      |
| aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg | 1551 |

|   |      |
|---|------|
| Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly |      |
| 480 485 490   |      |
| aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt | 1599 |
| Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly |      |
| 495 500 505   |      |
| ggg gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac | 1647 |
| Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp |      |
| 510 515 520   |      |
| ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa | 1695 |
| Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln |      |
| 525 530 535   |      |
| gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt | 1743 |
| Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe |      |
| 540 545 550 555   |      |
| gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt | 1791 |
| Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val |      |
| 560 565 570   |      |
| aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc | 1839 |
| Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe |      |
| 575 580 585   |      |
| gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt | 1887 |
| Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val |      |
| 590 595 600   |      |
| gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat | 1935 |
| Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr |      |
| 605 610 615   |      |
| gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag | 1983 |
| Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln |      |
| 620 625 630 635   |      |
| gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct | 2031 |
| Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala |      |
| 640 645 650   |      |
| ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa | 2079 |
| Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln |      |
| 655 660 665   |      |
| agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat | 2127 |
| Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp |      |
| 670 675 680   |      |
| gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca | 2175 |
| Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro |      |
| 685 690 695   |      |
| gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat | 2223 |
| Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr |      |
| 700 705 710 715   |      |



ctt gca cct gag tat gca g gtacagaaag cctttgattt tagttttgta 2272  
 Leu Ala Pro Glu Tyr Ala  
 720

caattgtgcc ttaattttga agttcatatt ttatatgtct gtatttggtg gttatagctg 2332  
 ttggttatta cttcaatatc atgcttcggt gttcagcaaa ttttaagtagt tcaccagagt 2392  
 aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gatactcaat 2452  
 tcctagatac atggctactt caaaattctt tgtggctatt tctttgcaat gttatatattt 2512  
 gctcttttca cgtgttttgt tgagttgggt gggggttttg ctgcatagtt cttggtgggt 2572  
 gatgcctcaa aagatatgtc gagccatttt tagacagttt accagagtct gactctcaat 2632  
 tatectttac gatgtgatga atactctggt tgcattaaat ctttgattgc tgtatatattg 2692  
 catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct 2752  
 atcccatttc cttgttggat cgggtgcattg aaacatcttt tgttaaaaact gttattttga 2812  
 tcgggtgtgt ttttatccat ttagcatcaa gacttttgca agcataaaac ttcctaaaat 2872  
 gttgcattga atgtgattag atggcatttg attagtgcta gtctatttgt ttgattatat 2932  
 ttaatgttac tctgtttctt accag ct act gga aga gtg aca acc aaa gtg 2983  
 Ala Thr Gly Arg Val Thr Thr Lys Val  
 725 730

gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga 3031  
 Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg  
 735 740 745

aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca 3079  
 Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr  
 750 755 760

tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att 3127  
 Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile  
 765 770 775

gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca 3175  
 Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr  
 780 785 790

gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg 3223  
 Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg  
 795 800 805 810

ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa 3271  
 Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln  
 815 820 825

tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt 3319  
 Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly  
 830 835 840

gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac 3367  
 Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn  
 845 850 855  
  
 gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa 3415  
 Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln  
 860 865 870  
  
 tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca 3463  
 Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser  
 875 880 885 890  
  
 atg gat tgc cgt taa cc 3480  
 Met Asp Cys Arg

<210> 45  
 <211> 3480  
 <212> DNA  
 <213> Glycine max  
  
 <220>  
 <221> CDS  
 <222> (79)..(2242), (2958)..(3478)  
  
 <223> Seq ID: rhg4\_Minsoy\_amplicon  
  
 <400> 45

atgtctctcc ccaaaaccct actttctctc ttccttctcc tcacgatccc cctagtaacc 60  
  
 gccgatgacg ccgcgggtg atg tcg aat ttt ctc aaa tcc ctc act cca ccg 111  
 Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro  
 1 5 10  
  
 ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc 159  
 Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile  
 15 20 25  
  
 caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cat 207  
 Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser His  
 30 35 40  
  
 tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc 255  
 Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu  
 45 50 55  
  
 cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct 303  
 Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser  
 60 65 70 75  
  
 ctc tcc aac ctt tct ttc ctc caa acc gtc tac tta aac cgc aac aac 351  
 Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn  
 80 85 90  
  
 ttc tcc tcc gtg tcc ccc acc gct ttc gcc tcc cta acc tcc ctc caa 399  
 Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln

| 95  | 100 | 105 |      |
|---|-----|-----|------|
| acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc |     |     | 447  |
| Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro |     |     |      |
| 110   | 115 | 120 |      |
| acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc |     |     | 495  |
| Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr |     |     |      |
| 125   | 130 | 135 |      |
| gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc |     |     | 543  |
| Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser |     |     |      |
| 140   | 145 | 150 | 155  |
| ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc |     |     | 591  |
| Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro |     |     |      |
| 160   | 165 | 170 |      |
| tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac |     |     | 639  |
| Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn |     |     |      |
| 175   | 180 | 185 |      |
| cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct |     |     | 687  |
| Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser |     |     |      |
| 190   | 195 | 200 |      |
| gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc ata |     |     | 735  |
| Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile |     |     |      |
| 205   | 210 | 215 |      |
| ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat |     |     | 783  |
| Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp |     |     |      |
| 220   | 225 | 230 | 235  |
| aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt |     |     | 831  |
| Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser |     |     |      |
| 240   | 245 | 250 |      |
| ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc |     |     | 879  |
| Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro |     |     |      |
| 255   | 260 | 265 |      |
| gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt |     |     | 927  |
| Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe |     |     |      |
| 270   | 275 | 280 |      |
| tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg |     |     | 975  |
| Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu |     |     |      |
| 285   | 290 | 295 |      |
| cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg |     |     | 1023 |
| Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp |     |     |      |
| 300   | 305 | 310 | 315  |
| aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc |     |     | 1071 |
| Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala |     |     |      |
| 320   | 325 | 330 |      |

|   |      |
|---|------|
| gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc | 1119 |
| Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr |      |
| 335 340 345   |      |
|   |      |
| atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc | 1167 |
| Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu |      |
| 350 355 360   |      |
|   |      |
| aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg | 1215 |
| Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu |      |
| 365 370 375   |      |
|   |      |
| cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg | 1263 |
| Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu |      |
| 380 385 390 395   |      |
|   |      |
| gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct | 1311 |
| Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala |      |
| 400 405 410   |      |
|   |      |
| ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act | 1359 |
| Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr |      |
| 415 420 425   |      |
|   |      |
| cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt | 1407 |
| Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly |      |
| 430 435 440   |      |
|   |      |
| aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg | 1455 |
| Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val |      |
| 445 450 455   |      |
|   |      |
| ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc | 1503 |
| Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val |      |
| 460 465 470 475   |      |
|   |      |
| aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg | 1551 |
| Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly |      |
| 480 485 490   |      |
|   |      |
| aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt | 1599 |
| Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly |      |
| 495 500 505   |      |
|   |      |
| ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac | 1647 |
| Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp |      |
| 510 515 520   |      |
|   |      |
| ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa | 1695 |
| Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln |      |
| 525 530 535   |      |
|   |      |
| gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt | 1743 |
| Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe |      |
| 540 545 550 555   |      |
|   |      |
| gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt | 1791 |
| Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val |      |

| 560  | 565 | 570 |      |
|--|-----|-----|------|
| aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc    |     |     | 1839 |
| Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe    |     |     |      |
| 575  | 580 | 585 |      |
| gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt    |     |     | 1887 |
| Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val    |     |     |      |
| 590  | 595 | 600 |      |
| gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat    |     |     | 1935 |
| Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr    |     |     |      |
| 605  | 610 | 615 |      |
| gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag    |     |     | 1983 |
| Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln    |     |     |      |
| 620  | 625 | 630 | 635  |
| gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct    |     |     | 2031 |
| Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala    |     |     |      |
| 640  | 645 | 650 |      |
| ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa    |     |     | 2079 |
| Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln    |     |     |      |
| 655  | 660 | 665 |      |
| agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat    |     |     | 2127 |
| Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp    |     |     |      |
| 670  | 675 | 680 |      |
| gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca    |     |     | 2175 |
| Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro    |     |     |      |
| 685  | 690 | 695 |      |
| gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat    |     |     | 2223 |
| Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr    |     |     |      |
| 700  | 705 | 710 | 715  |
| ctt gca cct gag tat gca g gtacagaaag cctttgattt tagttttgta         |     |     | 2272 |
| Leu Ala Pro Glu Tyr Ala  |     |     |      |
| 720  |     |     |      |
| caattgtgcc ttaattttga agttcatatt ttatatgtc gtatttggtg gttatagctg   |     |     | 2332 |
| ttggttatta cttcaatata atgcttcggg gttcagcaaa ttttaagtagt tcaccagagt |     |     | 2392 |
| aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gataactcaat |     |     | 2452 |
| tcctagatac atggctactt caaaattctt tgtggctatt tctttgcaat gttatatattt |     |     | 2512 |
| gctcttttca cgtgttttgt tgagttgggt gggggttttg ctgcatagtt cttgggtggtt |     |     | 2572 |
| gatgcctcaa aagatatgtc gagccatttt tagacagttt accagagtct gactctcaat  |     |     | 2632 |
| tatcctttac gatgtgatga atactctggg tgcattaaat ctttgattgc tgtatattgt  |     |     | 2692 |
| catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct  |     |     | 2752 |

atcccatcttc cttgttggat cgggtgcattg aaacatcttt tgttaaaact gttattttga 2812

tccgtgttgt ttttatccat ttagcatcaa gacttttgca agcataaaac ttcctaaaat 2872

gttgcattga atgtgattag atggcatttg attagtgcta gtctatttgt ttgattatat 2932

ttaatgttac tctgtttctt accag ct act gga aga gtg aca acc aaa gtg 2983  
 Ala Thr Gly Arg Val Thr Thr Lys Val  
 725 730

gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga 3031  
 Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg  
 735 740 745

aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca 3079  
 Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr  
 750 755 760

tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att 3127  
 Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile  
 765 770 775

gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca 3175  
 Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr  
 780 785 790

gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg 3223  
 Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg  
 795 800 805 810

ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa 3271  
 Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln  
 815 820 825

tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt 3319  
 Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly  
 830 835 840

gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac 3367  
 Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn  
 845 850 855

gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa 3415  
 Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln  
 860 865 870

tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca 3463  
 Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser  
 875 880 885 890

atg gat tgc cgt taa cc 3480  
 Met Asp Cys Arg

<210> 46  
 <211> 3480  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (79)..(2242),(2958)..(3478)  
 <223> Seq ID: rhg4\_Jack\_amplicon  
 <400> 46

atgtctctcc ccaaaaccct actttctctc ttccttctcc tcacgatccc cctagtaacc 60  
 gccgatgacg ccgcggtg atg tcg aat ttt ctc aaa tcc ctc act cca ccg 111  
 Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro  
 1 5 10  
 ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc 159  
 Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile  
 15 20 25  
 caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cag 207  
 Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln  
 30 35 40  
 tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc 255  
 Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu  
 45 50 55  
 cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct 303  
 Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser  
 60 65 70 75  
 ctc tcc aac ctt tct ttc ctc caa acc gtc tac tta aac cgc aac aac 351  
 Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn  
 80 85 90  
 ttc tcc tcc gtg tcc ccc acc gct ttc gcc tcc cta acc tcc ctc caa 399  
 Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln  
 95 100 105  
 acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc 447  
 Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro  
 110 115 120  
 acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc 495  
 Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr  
 125 130 135  
 gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc 543  
 Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser  
 140 145 150 155  
 ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc 591  
 Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro  
 160 165 170  
 tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac 639  
 Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn  
 175 180 185

|   |      |
|---|------|
| cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct | 687  |
| Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser |      |
| 190 195 200   |      |
| gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc ata | 735  |
| Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile |      |
| 205 210 215   |      |
| ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat | 783  |
| Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp |      |
| 220 225 230 235   |      |
| aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt | 831  |
| Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser |      |
| 240 245 250   |      |
| ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc | 879  |
| Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro |      |
| 255 260 265   |      |
| gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt | 927  |
| Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe |      |
| 270 275 280   |      |
| tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg | 975  |
| Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu |      |
| 285 290 295   |      |
| cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg | 1023 |
| Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp |      |
| 300 305 310 315   |      |
| aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc | 1071 |
| Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala |      |
| 320 325 330   |      |
| gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc | 1119 |
| Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr |      |
| 335 340 345   |      |
| atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc | 1167 |
| Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu |      |
| 350 355 360   |      |
| aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg | 1215 |
| Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu |      |
| 365 370 375   |      |
| cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg | 1263 |
| Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu |      |
| 380 385 390 395   |      |
| gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct | 1311 |
| Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala |      |
| 400 405 410   |      |
| ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act | 1359 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Leu | Leu | Gly | Lys | Pro | Leu | Ser | Pro | Gly | Gly | Gly | Pro | Ser | Gly | Thr | Thr |      |  |
|     |     |     | 415 |     |     |     |     | 420 |     |     |     |     | 425 |     |     |      |  |
| cct | tct | ggg | tct | tcg | acc | ggg | gga | agt | ggg | ggg | gaa | tcc | tca | aag | ggg | 1407 |  |
| Pro | Ser | Gly | Ser | Ser | Thr | Gly | Gly | Ser | Gly | Gly | Glu | Ser | Ser | Lys | Gly |      |  |
|     |     | 430 |     |     |     |     | 435 |     |     |     | 440 |     |     |     |     |      |  |
| aat | tct | tcg | gtg | tcg | cca | ggg | tgg | att | gct | ggg | ata | ggt | ggt | att | gtg | 1455 |  |
| Asn | Ser | Ser | Val | Ser | Pro | Gly | Trp | Ile | Ala | Gly | Ile | Val | Val | Ile | Val |      |  |
|     |     | 445 |     |     |     | 450 |     |     |     | 455 |     |     |     |     |     |      |  |
| ttg | ttt | ttt | att | gca | gtg | gtg | ttg | ttt | gtg | tct | tgg | aag | tgt | ttt | gtc | 1503 |  |
| Leu | Phe | Phe | Ile | Ala | Val | Val | Leu | Phe | Val | Ser | Trp | Lys | Cys | Phe | Val |      |  |
| 460 |     |     |     |     | 465 |     |     |     | 470 |     |     |     |     | 475 |     |      |  |
| aac | aag | ctg | cag | ggg | aag | ttc | agt | agg | ggt | aaa | ggg | cat | gaa | aat | ggg | 1551 |  |
| Asn | Lys | Leu | Gln | Gly | Lys | Phe | Ser | Arg | Val | Lys | Gly | His | Glu | Asn | Gly |      |  |
|     |     |     | 480 |     |     |     |     | 485 |     |     |     | 490 |     |     |     |      |  |
| aaa | gga | ggc | ttt | aaa | ctt | gat | gct | gtc | cat | ggt | tct | aat | gga | tat | ggg | 1599 |  |
| Lys | Gly | Gly | Phe | Lys | Leu | Asp | Ala | Val | His | Val | Ser | Asn | Gly | Tyr | Gly |      |  |
|     |     | 495 |     |     |     | 500 |     |     |     | 505 |     |     |     |     |     |      |  |
| ggg | ggt | cca | ggt | gag | ttg | caa | agc | cag | agc | agt | ggg | gat | cgc | agt | gac | 1647 |  |
| Gly | Val | Pro | Val | Glu | Leu | Gln | Ser | Gln | Ser | Ser | Gly | Asp | Arg | Ser | Asp |      |  |
|     |     | 510 |     |     |     | 515 |     |     |     | 520 |     |     |     |     |     |      |  |
| ctt | cat | gct | tta | gat | ggg | cca | aca | ttt | tct | atc | caa | ggt | ctt | cga | caa | 1695 |  |
| Leu | His | Ala | Leu | Asp | Gly | Pro | Thr | Phe | Ser | Ile | Gln | Val | Leu | Arg | Gln |      |  |
|     |     | 525 |     |     |     | 530 |     |     |     | 535 |     |     |     |     |     |      |  |
| gtg | acg | aat | aat | ttc | agc | gag | gag | aac | att | tta | ggc | agg | gga | ggg | ttt | 1743 |  |
| Val | Thr | Asn | Asn | Phe | Ser | Glu | Glu | Asn | Ile | Leu | Gly | Arg | Gly | Gly | Phe |      |  |
| 540 |     |     |     | 545 |     |     |     | 550 |     |     |     |     |     | 555 |     |      |  |
| gga | gta | ggt | tat | aag | ggg | gtg | ttg | cat | gat | gga | aca | aaa | att | gct | ggt | 1791 |  |
| Gly | Val | Val | Tyr | Lys | Gly | Val | Leu | His | Asp | Gly | Thr | Lys | Ile | Ala | Val |      |  |
|     |     |     | 560 |     |     |     |     | 565 |     |     |     | 570 |     |     |     |      |  |
| aag | agg | atg | gaa | tct | ggt | gca | atg | ggg | aac | aaa | ggg | cag | aaa | gag | ttc | 1839 |  |
| Lys | Arg | Met | Glu | Ser | Val | Ala | Met | Gly | Asn | Lys | Gly | Gln | Lys | Glu | Phe |      |  |
|     |     | 575 |     |     |     |     |     | 580 |     |     |     | 585 |     |     |     |      |  |
| gaa | gca | gag | att | gca | ctt | ctt | agt | aaa | ggt | agg | cat | aga | cat | ttg | ggt | 1887 |  |
| Glu | Ala | Glu | Ile | Ala | Leu | Leu | Ser | Lys | Val | Arg | His | Arg | His | Leu | Val |      |  |
|     |     | 590 |     |     |     |     | 595 |     |     | 600 |     |     |     |     |     |      |  |
| gct | ctt | cta | ggg | tat | tgc | atc | aat | ggc | aat | gaa | agg | ctt | ttg | gtg | tat | 1935 |  |
| Ala | Leu | Leu | Gly | Tyr | Cys | Ile | Asn | Gly | Asn | Glu | Arg | Leu | Leu | Val | Tyr |      |  |
|     |     | 605 |     |     |     | 610 |     |     |     | 615 |     |     |     |     |     |      |  |
| gag | tat | atg | cct | caa | ggg | aca | tta | aca | cag | cac | ctg | ttt | gag | tgg | cag | 1983 |  |
| Glu | Tyr | Met | Pro | Gln | Gly | Thr | Leu | Thr | Gln | His | Leu | Phe | Glu | Trp | Gln |      |  |
| 620 |     |     |     |     | 625 |     |     |     | 630 |     |     |     |     | 635 |     |      |  |
| gag | cat | ggg | tat | gct | cct | ttg | act | tgg | aag | caa | agg | gta | gta | ata | gct | 2031 |  |
| Glu | His | Gly | Tyr | Ala | Pro | Leu | Thr | Trp | Lys | Gln | Arg | Val | Val | Ile | Ala |      |  |
|     |     |     |     | 640 |     |     |     | 645 |     |     |     |     |     | 650 |     |      |  |

|   |      |
|---|------|
| ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa     | 2079 |
| Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln     |      |
| 655 660 665   |      |
| agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat     | 2127 |
| Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp     |      |
| 670 675 680   |      |
| gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca     | 2175 |
| Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro     |      |
| 685 690 695   |      |
| gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat     | 2223 |
| Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr     |      |
| 700 705 710 715   |      |
| ctt gca cct gag tat gca g gtacagaaag cctttgattt tagttttgta          | 2272 |
| Leu Ala Pro Glu Tyr Ala   |      |
| 720   |      |
| caattgtgcc ttaattttga agttcatatt ttatatgctc gtatttggtg gttatagctg   | 2332 |
| ttggttatta cttcaatatc atgcttcggt gttcagcaaa ttttaagtagt tcaccagagt  | 2392 |
| aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gataactcaat  | 2452 |
| tcctagatac atggctactt caaaattctt tgtggctatt tctttgcaat gttatatattt  | 2512 |
| gctcttttca cgtgttttgt tgagttgggt ggggggttttg ctgcatagtt cttgggtggtt | 2572 |
| gatgcctcaa aagatatgtc gagccatttt tagacagttt accagagtct gactctcaat   | 2632 |
| tatccctttac gatgtgatga atactctggt tgcattaaat ctttgattgc tgtatatattg | 2692 |
| catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct   | 2752 |
| atcccatttc cttgttggat cggtgcattg aaacatcttt tgttaaaact gttattttga   | 2812 |
| tcggtgttgt ttttatccat ttagcatcaa gacttttgca agcataaaac ttcctaaaat   | 2872 |
| gttgcatgga atgtgattag atggcatttg attagtgcta gtctatttgt ttgattatat   | 2932 |
| ttaatgttac tctgtttctt accag ct act gga aga gtg aca acc aaa gtg      | 2983 |
| Ala Thr Gly Arg Val Thr Thr Lys Val                                 |      |
| 725 730   |      |
| gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga     | 3031 |
| Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg     |      |
| 735 740 745   |      |
| aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca     | 3079 |
| Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr     |      |
| 750 755 760   |      |
| tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att     | 3127 |
| Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile     |      |
| 765 770 775   |      |

gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca 3175  
Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr  
780 785 790  
  
gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg 3223  
Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg  
795 800 805 810  
  
ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa 3271  
Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln  
815 820 825  
  
tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt 3319  
Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly  
830 835 840  
  
gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac 3367  
Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn  
845 850 855  
  
gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa 3415  
Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln  
860 865 870  
  
tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca 3463  
Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser  
875 880 885 890  
  
atg gat tgc cgt taa cc 3480  
Met Asp Cys Arg

<210> 47  
<211> 3480  
<212> DNA  
<213> Glycine max  
  
<220>  
<221> CDS  
<222> (79)..(2242), (2958)..(3478)  
<223> Seq ID: rhg4\_peking\_amplicon  
  
<400> 47

atgtctctcc ccaaaaccct actttctctc ttctttctcc tcacgatccc cctagtaacc 60  
  
gccgatgacg ccgcggtg atg tcg aat ttt ctc aaa tcc ctc act cca ccg 111  
Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro  
1 5 10  
  
ccc tcg ggc tgg tct gaa aca acc cca ttc tgc caa tgg aag ggt atc 159  
Pro Ser Gly Trp Ser Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile  
15 20 25  
  
caa tgc gat tca tcc agc cac gtg acc agc ata agc ctc gct tcg cag 207  
Gln Cys Asp Ser Ser Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln

| 30  | 35  | 40  |     |
|---|-----|-----|-----|
| tcc ctc acc gga aca ctc ccc tcg gat ctc aat tcc ctc tct caa ctc |     |     | 255 |
| Ser Leu Thr Gly Thr Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu |     |     |     |
| 45  | 50  | 55  |     |
| cgc act ctc tcc ctc caa gac aat tcc ctc acc ggc acc ctc cct tct |     |     | 303 |
| Arg Thr Leu Ser Leu Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser |     |     |     |
| 60  | 65  | 70  | 75  |
| ctc tcc aac ctt tct ttc ctc caa acc gtc tac ttc aac cgc aac aac |     |     | 351 |
| Leu Ser Asn Leu Ser Phe Leu Gln Thr Val Tyr Phe Asn Arg Asn Asn |     |     |     |
| 80  | 85  | 90  |     |
| ttc tcc tcc gtg tcc ccc acc gcc ttc gcc tcc cta acc tcc ctc caa |     |     | 399 |
| Phe Ser Ser Val Ser Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln |     |     |     |
| 95  | 100 | 105 |     |
| acc ctc agc ctc ggc tcc aac cct gct ctc caa ccc tgg tcc ttc ccc |     |     | 447 |
| Thr Leu Ser Leu Gly Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro |     |     |     |
| 110   | 115 | 120 |     |
| acc gac ctc act tcc tcc tct aac cta atc gac ctc gac ctc gcc acc |     |     | 495 |
| Thr Asp Leu Thr Ser Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr |     |     |     |
| 125   | 130 | 135 |     |
| gta tcc ctc acc ggt ccc ttg ccg gac att ttc gac aaa ttc cct tcc |     |     | 543 |
| Val Ser Leu Thr Gly Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser |     |     |     |
| 140   | 145 | 150 | 155 |
| ctt caa cac ctt cgc ctc tct tac aac aac ctc acc ggc aat tta ccc |     |     | 591 |
| Leu Gln His Leu Arg Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro |     |     |     |
| 160   | 165 | 170 |     |
| tcc tct ttc tcc gcc gcc aac aat ctc gaa acg ctc tgg ctc aac aac |     |     | 639 |
| Ser Ser Phe Ser Ala Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn |     |     |     |
| 175   | 180 | 185 |     |
| cag gcc gcc ggc ttg tcc ggt acc ctc ctc gtc ctc tcc aac atg tct |     |     | 687 |
| Gln Ala Ala Gly Leu Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser |     |     |     |
| 190   | 195 | 200 |     |
| gca tta aac cag tcc tgg ctc aat aag aac cag ttc acc ggt tcc att |     |     | 735 |
| Ala Leu Asn Gln Ser Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile |     |     |     |
| 205   | 210 | 215 |     |
| ccg gat tta tcg caa tgc acg gct ttg tct gac ttg cag ctc agg gat |     |     | 783 |
| Pro Asp Leu Ser Gln Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp |     |     |     |
| 220   | 225 | 230 | 235 |
| aac cag tta act ggt gtg gtt ccc gct tca ttg aca agt ctt cct agt |     |     | 831 |
| Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser |     |     |     |
| 240   | 245 | 250 |     |
| ttg aag aaa gtt tct ctg gat aat aat gag ctt cag ggg cct gtg ccc |     |     | 879 |
| Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro |     |     |     |
| 255   | 260 | 265 |     |

|   |      |
|---|------|
| gtg ttt ggg aaa ggt gtg aat gtt act ctc gat ggg att aat agt ttt | 927  |
| Val Phe Gly Lys Gly Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe |      |
| 270 275 280   |      |
| tgt ctt gat act cct ggg aat tgt gat ccc agg gtg atg gtt ttg ctg | 975  |
| Cys Leu Asp Thr Pro Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu |      |
| 285 290 295   |      |
| cag att gcc gag gca ttc ggg tat cca att cgg ttg gca gag tcg tgg | 1023 |
| Gln Ile Ala Glu Ala Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp |      |
| 300 305 310 315   |      |
| aag ggg aat gat ccg tgt gat ggt tgg aac tat gtt gtg tgt gct gcc | 1071 |
| Lys Gly Asn Asp Pro Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala |      |
| 320 325 330   |      |
| gga aag att att act gtc aat ttc gag aaa cag ggt ttg cag ggt acc | 1119 |
| Gly Lys Ile Ile Thr Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr |      |
| 335 340 345   |      |
| atc tcc cct gca ttt gcc aat ttg act gac ttg agg act ttg ttt ctc | 1167 |
| Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu |      |
| 350 355 360   |      |
| aat ggc aat aat ttg atc ggt tct ata cct gat agt ttg atc act ttg | 1215 |
| Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu |      |
| 365 370 375   |      |
| cct cag ctt cag act ctt gat gtg tct gac aac aac ctc tct gga ttg | 1263 |
| Pro Gln Leu Gln Thr Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu |      |
| 380 385 390 395   |      |
| gtt cct aag ttc cca cca aag gtg aag ttg gtg act gcg gga aat gct | 1311 |
| Val Pro Lys Phe Pro Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala |      |
| 400 405 410   |      |
| ttg ctt ggg aaa ccc ctt agt cct gga ggt gga cca agt gga act act | 1359 |
| Leu Leu Gly Lys Pro Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr |      |
| 415 420 425   |      |
| cct tct ggg tct tcg acc ggt gga agt ggt ggt gaa tcc tca aag ggt | 1407 |
| Pro Ser Gly Ser Ser Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly |      |
| 430 435 440   |      |
| aat tct tcg gtg tcg cca ggt tgg att gct ggt ata gtt gtt att gtg | 1455 |
| Asn Ser Ser Val Ser Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val |      |
| 445 450 455   |      |
| ttg ttt ttt att gca gtg gtg ttg ttt gtg tct tgg aag tgt ttt gtc | 1503 |
| Leu Phe Phe Ile Ala Val Val Leu Phe Val Ser Trp Lys Cys Phe Val |      |
| 460 465 470 475   |      |
| aac aag ctg cag ggg aag ttc agt agg gtt aaa ggt cat gaa aat ggg | 1551 |
| Asn Lys Leu Gln Gly Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly |      |
| 480 485 490   |      |
| aaa gga ggc ttt aaa ctt gat gct gtc cat gtt tct aat gga tat ggt | 1599 |
| Lys Gly Gly Phe Lys Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly |      |

| 495   | 500 | 505 |      |
|---|-----|-----|------|
| ggt gtt cca gtt gag ttg caa agc cag agc agt ggt gat cgc agt gac |     |     | 1647 |
| Gly Val Pro Val Glu Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp |     |     |      |
| 510   | 515 | 520 |      |
| ctt cat gct tta gat ggt cca aca ttt tct atc caa gtt ctt cga caa |     |     | 1695 |
| Leu His Ala Leu Asp Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln |     |     |      |
| 525   | 530 | 535 |      |
| gtg acg aat aat ttc agc gag gag aac att tta ggc agg gga ggg ttt |     |     | 1743 |
| Val Thr Asn Asn Phe Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe |     |     |      |
| 540   | 545 | 550 | 555  |
| gga gta gtt tat aag ggg gtg ttg cat gat gga aca aaa att gct gtt |     |     | 1791 |
| Gly Val Val Tyr Lys Gly Val Leu His Asp Gly Thr Lys Ile Ala Val |     |     |      |
| 560   | 565 | 570 |      |
| aag agg atg gaa tct gtt gca atg ggg aac aaa ggt cag aaa gag ttc |     |     | 1839 |
| Lys Arg Met Glu Ser Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe |     |     |      |
| 575   | 580 | 585 |      |
| gaa gca gag att gca ctt ctt agt aaa gtt agg cat aga cat ttg gtt |     |     | 1887 |
| Glu Ala Glu Ile Ala Leu Leu Ser Lys Val Arg His Arg His Leu Val |     |     |      |
| 590   | 595 | 600 |      |
| gct ctt cta ggg tat tgc atc aat ggc aat gaa agg ctt ttg gtg tat |     |     | 1935 |
| Ala Leu Leu Gly Tyr Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr |     |     |      |
| 605   | 610 | 615 |      |
| gag tat atg cct caa ggt aca tta aca cag cac ctg ttt gag tgg cag |     |     | 1983 |
| Glu Tyr Met Pro Gln Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln |     |     |      |
| 620   | 625 | 630 | 635  |
| gag cat ggg tat gct cct ttg act tgg aag caa agg gta gta ata gct |     |     | 2031 |
| Glu His Gly Tyr Ala Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala |     |     |      |
| 640   | 645 | 650 |      |
| ttg gat gta gcg cgg ggg gtg gaa tac ttg cac agt tta gct cag caa |     |     | 2079 |
| Leu Asp Val Ala Arg Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln |     |     |      |
| 655   | 660 | 665 |      |
| agc ttc att cat aga gac tta aaa ccc tca aac ata cta cta ggc gat |     |     | 2127 |
| Ser Phe Ile His Arg Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp |     |     |      |
| 670   | 675 | 680 |      |
| gac atg aga gca aag gtt gct gat ttt ggg ttg gtt aaa aat gca cca |     |     | 2175 |
| Asp Met Arg Ala Lys Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro |     |     |      |
| 685   | 690 | 695 |      |
| gat ggg aag tat tct gtt gag aca cgg ttg gct gga aca ttt gga tat |     |     | 2223 |
| Asp Gly Lys Tyr Ser Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr |     |     |      |
| 700   | 705 | 710 | 715  |
| ctt gca cct gag tat gca g gtacagaaag cctttgattt tagttttgta      |     |     | 2272 |
| Leu Ala Pro Glu Tyr Ala   |     |     |      |
| 720   |     |     |      |

|  |      |
|--|------|
| caattgtgcc ttaatTTTga agttcatatt ttatatgctc gtatttggtg gttatagctg    | 2332 |
| ttggtttagta cttcaatatc atgcttcggt gttcagcaaa ttttaagtagt tcaccagagt  | 2392 |
| aatcgctcac atacaaaaaa aaagtagaaa gagttgaagg gaaaataatt gatactcaat    | 2452 |
| tcctagatac atggctactt caaaattctt tgtggctatt tctttgcaat gttatatTTT    | 2512 |
| gctctTTTca cgtgTTTTgt tgagttgggt gggggTTTTg ctgcatagtt cttggtgggt    | 2572 |
| gatgcctcaa aagatatgtc gagccatttt tagacagttt accagagtct gactctcaat    | 2632 |
| tatcctttac gatgtgatga atactctggt tgcattaaat ctttgattgc tgtatattgt    | 2692 |
| catgggctta ggtggtagtt ctctgtcgca actaatcact gttgtggaat ttatcattct    | 2752 |
| atccccatttc cttgttggat cgggtgcattg aaacatcttt tgttaaaaact gttatTTTga | 2812 |
| tcgggtgttgt ttttatccat ttagcatcaa gactTTTgca agcataaaac ttcctaaaat   | 2872 |
| gttgcattga atgtgattag atggcatttg attagtgcta gtctatttgt ttgattatat    | 2932 |
| ttaatgttac tctgtttctt accag ct act gga aga gtg aca acc aaa gtg       | 2983 |
| Ala Thr Gly Arg Val Thr Thr Lys Val                                  |      |
| 725 730  |      |
| gat gtt tat gca ttt gga gta gtt ctg atg gaa ctt atc acc ggt aga      | 3031 |
| Asp Val Tyr Ala Phe Gly Val Val Leu Met Glu Leu Ile Thr Gly Arg      |      |
| 735 740 745  |      |
| aag gca ttg gat gat act gtg cca gat gaa agg tct cac ttg gtg aca      | 3079 |
| Lys Ala Leu Asp Asp Thr Val Pro Asp Glu Arg Ser His Leu Val Thr      |      |
| 750 755 760  |      |
| tgg ttc cgt agg gta cta att aac aag gaa aac att cca aag gca att      | 3127 |
| Trp Phe Arg Arg Val Leu Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile      |      |
| 765 770 775  |      |
| gat caa att ctc aat cca gat gag gaa acc atg gga agc ata tat aca      | 3175 |
| Asp Gln Ile Leu Asn Pro Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr      |      |
| 780 785 790  |      |
| gtg gcc gag ctg gca ggc cat tgc act gct cgc gaa cca tac caa agg      | 3223 |
| Val Ala Glu Leu Ala Gly His Cys Thr Ala Arg Glu Pro Tyr Gln Arg      |      |
| 795 800 805 810  |      |
| ccg gat atg ggt cat gca gtg aac gtc ttg gtt cct ctt gtg gag caa      | 3271 |
| Pro Asp Met Gly His Ala Val Asn Val Leu Val Pro Leu Val Glu Gln      |      |
| 815 820 825  |      |
| tgg aaa cct act agc cat gat gaa gaa gag gaa gac ggc tct ggc ggt      | 3319 |
| Trp Lys Pro Thr Ser His Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly      |      |
| 830 835 840  |      |
| gac ctt cat atg agc ctt cct caa gct cta cga agg tgg caa gcc aac      | 3367 |
| Asp Leu His Met Ser Leu Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn      |      |
| 845 850 855  |      |

gaa ggc act tcc tca ata ttt aat gac att tcc atc tca caa acc caa 3415  
 Glu Gly Thr Ser Ser Ile Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln  
 860 865 870

tca agc atc tcc tct aaa cct gca ggg ttt gca gac tcc ttt gat tca 3463  
 Ser Ser Ile Ser Ser Lys Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser  
 875 880 885 890

atg gat tgc cgt taa cc 3480  
 Met Asp Cys Arg

<210> 48  
 <211> 30  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_forward

<400> 48

atgtctctcc ccaaaaccct actttctctc 30

<210> 49  
 <211> 30  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_reverse

<400> 49

ggttaacggc aatccattga atcaaaggag 30

<210> 50  
 <211> 2685  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg4\_A3244\_amplicon\_cds

<400> 50

atgtcgaatt ttctcaaata cctcactcca ccgccctcgg gctgggtctga aacaacccca 60

ttctgccaat ggaagggtat ccaatgcgat tcatccagcc acgtgaccag cataagcctc 120

gcttcgcatt ccctcaccgg aacactcccc tcggatctca attccctctc tcaactccgc 180

actctctccc tccaagacaa ttccctcacc ggcaccctcc cttctctctc caacctttct 240

ttctccaaa ccgtctactt aaaccgcaac aacttctcct ccgtgtcccc caccgctttc 300

gcctccctaa cctccctcca aaccctcagc ctcggctcca accctgctct ccaaccctgg 360

tccttcccca ccgacctcac ttctcctctt aacctaatcg acctcgacct cgccaccgta 420



tccctcaccg gtcccttgcc ggacattttc gacaaattcc cttcccttca acaccttcgc 480  
ctctcttaca acaacctcac cggcaattta ccttcctctt tctccgccgc caacaatctc 540  
gaaacgctct ggctcaacaa ccaggccgcc ggcttgtccg gtaccctcct cgtcctctcc 600  
aacatgtctg cattaaacca gtcttggtc aataagaacc agttcacccg ttccataccg 660  
gatttatcgc aatgcacggc tttgtctgac ttgcagctca gggataacca gttaactggt 720  
gtggttcccg cttcattgac aagtcttcct agtttgaaga aagtttctct ggataataat 780  
gagcttcagg ggctgtgcc cgtgtttggg aaagggtgta atgttactct cgatgggatt 840  
aatagttttt gtcttgatac tcctgggaat tgtgatccca gggatgatgt tttgctgcag 900  
attgccgagg cattcgggta tccaattcgg ttggcagagt cgtggaaggg gaatgatccg 960  
tgtgatgggt ggaactatgt tgtgtgtgct gccggaaaga ttattactgt caatttcgag 1020  
aaacagggtt tgcagggtac catctccctt gcatttgcca atttgactga cttgaggact 1080  
ttgtttctca atggcaataa tttgatcggc tctataacct atagtttgat cactttgcct 1140  
cagcttcaga ctcttgatgt gtctgacaac aacctctctg gattgggtcc taagttccca 1200  
ccaaagggtga agttggtgac tgcgggaaat gctttgcttg ggaaaccctt tagtcctgga 1260  
ggtggaccaa gtggaactac tccttctggg tcttcgaccg gtggaagtgg tgggtgaatcc 1320  
tcaaagggtta attcttcggc gtccgcaggc tggattgctg gtatagttgt tattgtgttg 1380  
ttttttattg cagtgggtgt gtttgtgtct tggaaagtgt ttgtcaacaa gctgcagggg 1440  
aagttcagta ggggttaaagg tcatgaaaat gggaaaggag gctttaaact tgatgctgtc 1500  
catgtttcta atggatatgg tgggtgtcca gttgagttgc aaagccagag cagtgggtgat 1560  
cgcagtgacc ttcattgctt agatgggtcca acattttcta tccaagttct tcgacaagtg 1620  
acgaataatt tcagcgagga gaacatttta ggcaggggag gggttgaggt agtttataag 1680  
ggggtgttgc atgatggaac aaaaattgct gttaaagga tggaaatctgt tgcaatgggg 1740  
aacaagggtc agaaagaggt cgaagcagag attgcacttc ttagtaaagt taggcataga 1800  
catttggttg ctcttctagg gtattgcac aatggcaatg aaaggctttt ggtgtatgag 1860  
tatatgcctc aaggtacatt aacacagcac ctgtttgagt ggcaggagca tgggtatgct 1920  
cctttgactt ggaagcaaag ggtagtaata gctttggatg tagcgcgggg ggtggaatac 1980  
ttgcacagtt tagctcagca aagcttcatt catagagact taaaaccctc aaacatacta 2040  
ctaggcgatg acatgagagc aaagggtgct gattttgggt tgggttaaaaa tgcaccagat 2100  
gggaagtatt ctgttgagac acggttggct ggaacatttg gatattctgc acctgagtat 2160

gcagctactg gaagagtgac aaccaaagtg gatgtttatg catttggagt agttctgatg 2220  
gaacttatca ccggtagaaa ggcattggat gatactgtgc cagatgaaag gtctcacttg 2280  
gtgacatggg tccgtagggt actaat AAC aaggaaaaca ttccaaaggc aattgatcaa 2340  
attctcaatc cagatgagga aacctaggga agcatatata cagtggccga gctggcaggc 2400  
cattgcactg ctcgcgaacc ataccaaagg ccggatatgg gtcatgcagt gaacgtcttg 2460  
gttcctcttg tggagcaatg gaaacctact agccatgatg agaagagga agacggctct 2520  
ggcggtgacc ttcatatgag ccttctcaa gctctacgaa ggtggcaagc caacgaaggc 2580  
acttctcaa tatttaatga catttccatc tcacaaacct aatcaagcat ctcctctaaa 2640  
cctgcagggt ttgcagactc ctttgattca atggattgcc gttaa 2685

<210> 51  
<211> 2685  
<212> DNA  
<213> Glycine max

<223> Seq ID: rhg4\_Minsoy\_amplicon\_cds

<400> 51

atgtcgaatt ttctcaaact cctcactcca ccgccctcgg gctgggtctga aacaacccca 60  
ttctgccaat ggaagggat ccaatgcgat tcattccagc acgtgaccag cataagcctc 120  
gcttcgcatt cctcaccgg aacctcccc tcggatctca attcctctc tcaactccgc 180  
actctctccc tccaagacaa ttccctcacc ggcacctcc cttctctctc caacctttct 240  
ttctccaaa ccgtctactt aaaccgcaac aacttctcct ccgtgtcccc caccgctttc 300  
gcctccctaa cctccctcca aacctcagc ctgggtcca accctgctct ccaacctggt 360  
tccttcccca ccgacctcac ttctctctc aacctaatcg acctcgacct cgccaccgta 420  
tcctcaccg gtcccttgcc ggacattttc gacaaattcc ctcccttca acaccttcgc 480  
ctctcttaca acaacctcac cggcaattta cctctctctt tctccgccgc caacaatctc 540  
gaaacgtctt ggctcaacaa ccaggccgcc ggcttgctcg gtacctctct cgtctctctc 600  
aacatgtctg cattaaacca gtctggctc aataagaacc agttcaccgg ttccataccg 660  
gatttatcgc aatgcacggc tttgtctgac ttgcagctca gggataacca gttaactggg 720  
gtggttcccg cttcattgac aagtcttct agtttgaaga aagtttctct ggataataat 780  
gagcttcagg ggcctgtgcc cgtgtttggg aaagggtgta atgttactct cgatgggatt 840  
aatagttttt gtcttgatac tcctgggaat tgtgatccca gggatgatgg tttgctgcag 900

attgccgagg cattcgggta tccaattcgg ttggcagagt cgtggaaggg gaatgatccg 960  
tgtgatgggt ggaactatgt tgttgtgtgt gccggaaaga ttattactgt caatttcgag 1020  
aaacaggggt tgcaggggtac catctccctt gcatttgcca atttgactga cttgaggact 1080  
ttgtttctca atggcaataa ttgatcgggt tctatacctg atagtgtgat cactttgcct 1140  
cagcttcaga ctcttgatgt gtctgacaac aacctctctg gattgggtcc taagttccca 1200  
ccaaagggtga agttgggtgac tgcgggaaat gctttgcttg ggaaaccctt tagtcctgga 1260  
gggtggaccaa gtggaactac tccttctggg tcttcgaccg gtggaagtgg tggatgaatcc 1320  
tcaaagggtta attcttcgggt gtcgccaggt tggattgctg gtatagtgtt tattgtgttg 1380  
ttttttattg cagtgggtgtt gtttgtgtct tggagtggtt ttgtcaaca gctgcagggg 1440  
aagttcagta ggggttaaagg tcatgaaaat gggaaaggag gctttaaact tgatgctgtc 1500  
catgtttcta atggatatgg tgggtgttcca gttgagttgc aaagccagag cagtgggtgat 1560  
cgcagtgacc ttcattgcttt agatgggtcca acattttcta tccaagttct tcgacaagtg 1620  
acgaataatt tcagcgagga gaacatttta ggcaggggag ggtttggagt agtttataag 1680  
gggggtgttg atgatggaac aaaaattgct gtttaagagga tggaaatctgt tgcaatgggg 1740  
aacaagggtc agaaagagtt cgaagcagag attgcacttc ttagtaaagt taggcataga 1800  
catttggttg ctcttctagg gtattgcac aatggcaatg aaaggctttt ggtgtatgag 1860  
tatatgcctc aaggtagatt aacacagcac ctgtttgagt ggcaggagca tgggtatgct 1920  
cctttgactt ggaagcaaag gtagtaata gctttggatg tagcgcgggg ggtggaatac 1980  
ttgcacagtt tagctcagca aagcttcatt catagagact taaaaccctc aaacatacta 2040  
ctaggcgatg acatgagagc aaagggtgct gattttgggt tgggttaaaaa tgcaccagat 2100  
gggaagtatt ctgttgagac acgggtgggt ggaacatttg gatattcttg acctgagtat 2160  
gcagctactg gaagagtgac aaccaagtgt gatgtttatg catttggagt agttctgatg 2220  
gaacttatca ccggtagaaa ggcattggat gatactgtgc cagatgaaag gtctcacttg 2280  
gtgacatgggt tccgtaggggt actaattaac aaggaaaaca ttccaaaggc aattgatcaa 2340  
attctcaatc cagatgagga aaccatggga agcatatata cagtggccga gctggcaggc 2400  
cattgcactg ctgcgcaacc ataccaaagg ccggatatgg gtcattgcagt gaacgtcttg 2460  
gttcctcttg tggagcaatg gaaacctact agcatgatg aagaagagga agacggctct 2520  
ggcggtgacc ttcatatgag ccttcctcaa gctctacgaa ggtggcaagc caacgaaggc 2580  
acttcctcaa tatttaatga catttccatc tcacaaaccc aatcaagcat ctctctctaa 2640

cctgcagggt ttgcagactc ctttgattca atggattgcc gttaa 2685

<210> 52

<211> 2685

<212> DNA

<213> Glycine max

<223> Seq ID: rhg4\_Jack\_amplicon\_cds

<400> 52

atgtcgaatt ttctcaaadc cctcactcca ccgccctcgg gctgggtctga aacaacccca 60  
 ttctgccaat ggaagggat ccaatgcgat tcatccagcc acgtgaccag cataagcctc 120  
 gcttcgcagt ccctcaccgg aacactcccc tcggatctca attccctctc tcaactccgc 180  
 actctctccc tccaagacaa ttccctcacc ggacccctcc cttctctctc caacctttct 240  
 ttctctcaaa ccgtctactt aaaccgcaac aactttctct ccgtgtcccc caccgctttc 300  
 gcctccctaa cctccctcca aaccctcagc ctcgggtcca accctgctct ccaaccctgg 360  
 tccttcccca ccgacctcac ttctctctct aacctaatcg acctcgacct cgccaccgta 420  
 tccctcaccg gtcccttgcc ggacattttc gacaaattcc cttcccttca acaccttcgc 480  
 ctctcttaca acaacctcac cggcaattta ccctctctct tctccgccgc caacaatctc 540  
 gaaacgctct ggctcaacaa ccaggccgcc ggcttggtcc gtacctctct cgtcctctcc 600  
 aacatgtctg cattaaacca gtctgggtc aataagaacc agttcaccgg ttccataccg 660  
 gatttatcgc aatgcacggc tttgtctgac ttgcagctca gggataacca gttaactggg 720  
 gtgggttccc cttcattgac aagtcttct agtttgaaga aagtttctct ggataataat 780  
 gagcttcagg gccctgtgcc cgtgtttggg aaagggtgtga atgttactct cgatgggatt 840  
 aatagttttt gtcttgatac tcttggaat tgtgatccca gggatgggt tttgctgcag 900  
 attgccgagg cattcgggta tccaattcgg ttggcagagt cgtggaaggg gaatgatccg 960  
 tgtgatgggt ggaactatgt tgtgtgtgct gccggaaaga ttattactgt caatttcgag 1020  
 aaacagggtt tgcagggtac catctccct gcatttgcca atttgactga cttgaggact 1080  
 ttgtttctca atggcaataa ttgatcggg tctatacctg atagtttgat cactttgcct 1140  
 cagcttcaga ctcttgatgt gtctgacaac aacctctctg gattgggttc taagttccca 1200  
 ccaaagggtga agttgggtgac tgcgggaaat gctttgcttg ggaacccct tagtcctgga 1260  
 ggtggaccaa gtggaactac tccttctggg tcttcgaccg gtggaagtgg tggatgaatcc 1320  
 tcaaagggtta attcttcggg gtcgccaggg tggattgctg gtatagttgt tattgtgttg 1380

ttttttattg cagtgggtgtt gtttgtgtct tggaagtgtt ttgtcaacaa gctgcagggg 1440  
 aagttcagta ggggttaaagg tcatgaaaat gggaaaggag gctttaaact tgatgctgtc 1500  
 catgttttcta atggatatgg tgggtgttcca gttgagttgc aaagccagag cagtgggtgat 1560  
 cgcagtgacc ttcattgcttt agatgggtcca acatttttcta tccaagttct tcgacaagtg 1620  
 acgaataatt tcagcgagga gaacatttta ggcaggggag ggtttggagt agtttataag 1680  
 ggggtgttgc atgatggaac aaaaattgct gttaagagga tggaatctgt tgcaatgggg 1740  
 aacaaagggtc agaaagagtt cgaagcagag attgcacttc ttagtaaagt taggcataga 1800  
 catttgggtg ctcttctagg gtattgcac c aatggcaatg aaaggctttt ggtgtatgag 1860  
 tatatgcctc aagggtacatt aacacagcac ctgtttgagt ggcaggagca tgggtatgct 1920  
 cctttgactt ggaagcaaag ggtagtaata gctttggatg tagcgcgggg ggtggaatac 1980  
 ttgcacagtt tagctcagca aagcttcatt catagagact taaaaccctc aaacatacta 2040  
 ctaggcgatg acatgagagc aaaggttgct gattttgggt tgggttaaaaa tgcaccagat 2100  
 gggaagtatt ctgttgagac acggttggct ggaacatttg gatattcttg acctgagtat 2160  
 gcagctactg gaagagtgac aaccaaagtg gatgtttatg catttggagt agttctgatg 2220  
 gaacttatca ccggtagaaa ggcattggat gatactgtgc cagatgaaag gtctcacttg 2280  
 gtgacatgggt tccgtaggggt actaattaac aaggaaaaca ttccaaaggc aattgatcaa 2340  
 attctcaatc cagatgagga aaccatggga agcatatata cagtggccga gctggcaggc 2400  
 cattgcactg ctgcggaacc ataccaaagg ccggatatgg gtcattgcagt gaacgtcttg 2460  
 gttcctcttg tggagcaatg gaaacctact agccatgatg aagaagagga agacggctct 2520  
 ggcggtgacc ttcattatgag ccttcctcaa gctctacgaa ggtggcaagc caacgaaggc 2580  
 acttcctcaa tatttaatga catttccatc tcacaaacct aatcaagcat ctctctctaa 2640  
 cctgcaggggt ttgcagactc ctttgattca atggattgcc gttaa 2685

<210> 53  
 <211> 2685  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: rhg4\_peking\_amplicon\_cds

<400> 53

atgtcgaatt ttctcaaact cctcactcca ccgccctcgg gctggtctga aacaacccca 60

ttctgccaat ggaaggggat ccaatgcgat tcatccagcc acgtgaccag cataagcctc 120  
 gcttcgcagt ccttcaccgg aacactcccc tcggatctca attccctctc tcaactccgc 180  
 actctctccc tccaagacaa ttccctcacc ggcaccctcc cttctctctc caacccttct 240  
 ttcttccaaa cgtctactt caaccgcaac aacttctcct cgtgttcccc caccgccttc 300  
 gcctccctaa cctccctcca aaccctcagc ctgggtcca accctgctct ccaaccctgg 360  
 tccttcccca cgcacctcac ttctcctctt aacctaatcg acctcgacct cgccaccgta 420  
 tccctcaccg gtcccttgcc ggacattttc gacaaattcc cttcccttca acaccttcgc 480  
 ctctcttaca acaacctcac cggcaattta cctcctctt tctccgcgc caacaatctc 540  
 gaaacgctct ggctcaacaa ccaggccgcc ggcttggtcc gtaccctcct cgtcctctcc 600  
 aacatgtctg cattaaacca gtcttggtc aataagaacc agttcaccgg ttccattccg 660  
 gatttatcgc aatgcacggc tttgtctgac ttgcagctca gggataacca gttaactggt 720  
 gtggttcccc cttcattgac aagtcttctt agtttgaaga aagtttctct ggataataat 780  
 gagcttcagg ggcctgtgcc cgtgtttggg aaagggtgta atgttactct cgatgggatt 840  
 aatagttttt gtcttgatac tcctgggaat tgtgatccca gggatgatgg tttgctgcag 900  
 attgccgagg cattcgggta tccaattcgg ttggcagagt cgtggaagg gaatgatccg 960  
 tgtgatgggt ggaactatgt tgtgtgtgct gccggaaga ttattactgt caatttcgag 1020  
 aaacaggggt tgcaggggtac catctccctt gcatttgcca atttgactga cttgaggact 1080  
 ttgtttctca atggcaataa tttgatcgg tctatacctg atagtttgat cactttgcct 1140  
 cagcttcaga ctcttgatgt gtctgacaac aacctctctg gattgggttc taagttccca 1200  
 ccaaagggtga agttggtgac tgcgggaaat gctttgcttg ggaaaccct tagtcctgga 1260  
 ggtggaccaaa gtggaactac tccttctggg tcttcgaccg gtggaagtgg tgggtgaatcc 1320  
 tcaaagggtta attcttcggg gtccgcagg ttgattgctg gtatagttgt tattgtgttg 1380  
 ttttttattg cagtgggtgt gtttgtgtct tggaaagtgt ttgtcaacaa gctgcagggg 1440  
 aagttcagta gggttaaagg tcatgaaaat gggaaaggag gctttaaact tgatgctgtc 1500  
 catgtttcta atggatatgg tgggtgtcca gttgagttgc aaagccagag cagtgggtgat 1560  
 cgcagtgacc ttcattgctt agatggtcca acattttcta tccaagttct tcgacaagtg 1620  
 acgaataatt tcagcgagga gaacatttta ggcaggggag ggtttggagt agtttataag 1680  
 ggggtgttgc atgatggaac aaaaattgct gttaagagga tggaaatctgt tgcaatgggg 1740  
 aacaaagggtc agaaagagtt cgaagcagag attgcacttc ttagtaaagt taggcataga 1800

catttggttg ctcttctagg gtattgcac aatggcaatg aaaggctttt ggtgtatgag 1860  
 tatatgcctc aaggtacatt aacacagcac ctgtttgagt ggcaggagca tgggtatgct 1920  
 cctttgactt ggaagcaaag ggtagtaata gctttggatg tagcgcgggg ggtggaatac 1980  
 ttgcacagtt tagctcagca aagcttcatt catagagact taaaaccctc aaacatacta 2040  
 ctaggcgatg acatgagagc aaaggttgct gattttgggt tggttaaaaa tgcaccagat 2100  
 gggaagtatt ctgttgagac acggttggct ggaacatttg gatatcttgc acctgagtat 2160  
 gcagctactg gaagagtgc aaccaaagtg gatgtttatg catttgagat agttctgatg 2220  
 gaacttatca ccggtagaaa ggcattggat gatactgtgc cagatgaaag gtctcacttg 2280  
 gtgacatggt tccgtagggt actaattaac aaggaaaaca ttccaaaggc aattgatcaa 2340  
 attctcaatc cagatgagga aaccatggga agcatatata cagtggccga gctggcaggc 2400  
 cattgcactg ctgcgaacc ataccaaagg ccggatatgg gtcattgcagt gaacgtcttg 2460  
 gttcctcttg tggagcaatg gaaacctact agccatgatg aagaagagga agacggctct 2520  
 ggcggtgacc ttcatatgag ccttcctcaa gctctacgaa ggtggcaagc caacgaaggc 2580  
 acttcctcaa tatttaatga catttccatc tcacaaacct aatcaagcat ctctctctaa 2640  
 cctgcagggt ttgcagactc ctttgattca atggattgcc gttaa 2685

<210> 54  
 <211> 120  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_289711\_11

<400> 54

aaaccttgac gttgttgtct ttgttttcat taataaaaaa atcatataag gtccacctta 60  
 tcccacgaca caacatatat atatacttcc ttaattaccg ggtgattggg acaatattcc 120

<210> 55  
 <211> 128  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_236585\_14

<400> 55

agtccgggag attagttgca gtaaaaaagt ccgggtgatt agagttaaag aatatatgta 60  
 aagatatctt aataaaaaa aaacaaaaaa caaaaaagtt agatcaggca atcagattca 120

gatctttca 128

<210> 56  
 <211> 129  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_168772\_13

<400> 56

tttgcattgt ttcaatttat ttccatgggt tgtctattaa taaactgggt caacctctta 60  
 accccatgat gattatatat acgttttgcg tgtgtgtgtg tgatcactca atgtctgttg 120  
 gttgaaatt 129

<210> 57  
 <211> 131  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_332420\_21

<400> 57

gagaatctgc aactgaacca aatgattaaa ctaaaaaac aagctagaaa agaaaagtaa 60  
 agaaaaaaag agattgtttt actagtcccc tcctatgtag ttgaaaccag tctgctgttc 120  
 cattcctaag t 131

<210> 58  
 <211> 135  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_228126\_18

<400> 58

atagctctgt tgcaaaggaa gatggtggag cttcaacatg atctggcaat tgcaaaggat 60  
 cgtcttgccg gttgtcaegc tgctgctgct gctgctacta ctactatccc ttctcctgat 120  
 atcttgcattg ccaat 135

<210> 59  
 <211> 137  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_139723\_11



&lt;400&gt; 59

ttgcattcaa attcatggaa ctaccatttt ttcttagcct ccccttcag gatacatcac 60

acacacaccg tgaaagttaa aaagttaaaa ggtagaatt ttgacatag cagttatgtt 120

tcatgcacac atggtga 137

&lt;210&gt; 60

&lt;211&gt; 138

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_280585\_14

&lt;400&gt; 60

tttacaagtg catcatttaa cttctcatat attatatata aaaagagggg taaaaggaaa 60

tttatcttat cttattgatc ataatttctc atataattaa tcaaacgcta cgtacaggat 120

ctttaaattg aggcctaaa 138

&lt;210&gt; 61

&lt;211&gt; 139

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_70509\_14

&lt;400&gt; 61

cctatgaaga atacaccac gttgaaatac atgttggtgt tgttgagcgc gccagccga 60

gagtgccggt ccacgagtat cccaacgtg catggcgcat gcgcttgaaa cctagtattc 120

atcttcctga tggaggctg 139

&lt;210&gt; 62

&lt;211&gt; 139

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_50537\_17

&lt;400&gt; 62

aaaccaaca taattccaac ttcaaaattc actcaataaa aagtttaaca tgtaaattta 60

cttggaaca aaactcataa ccaataataa taataataaa agaaatcagt tttatagcat 120

taatttggga tgctctgct 139

&lt;210&gt; 63

<211> 139  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_231556\_17

<400> 63

agcccttcca caaactagag cgtatgaagt gaaatatcgt caaacttttc atatctgcca 60  
 atgctctcaa ttatttttaa tttcattcaa gaagaagaag aagaaatact tcacatttac 120  
 tggaagtgtt tcggcagaa 139

<210> 64  
 <211> 141  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_117057\_11

<400> 64

aaagacggaa cagcgtcaaa taaacgggga gagagagagg gttaagggca gatcaggaag 60  
 agacccatct tcgctgagga tgccgtgagg gaagttgcga atgggagaag agaggggtga 120  
 attgtagagc gtgtttccgt c 141

<210> 65  
 <211> 142  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_23092\_13

<400> 65

tcaataggta ctggcacaag acacctagta atatgcgaaa tctcttatgt ttgtatcacc 60  
 aaaatggaca atgagaggac ataacaacaa caacaccacc aaaaccttat ccactagga 120  
 atgagaggac ataaagggt aa 142

<210> 66  
 <211> 144  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_297741\_14

<400> 66

tttataaatc tgtccagcca caaaataat gttccaggtg tcaaaaacta tgctctaacc 60

ttttttatattt atttttttatt ttgcatttttg aaaaaacaga ctctgttttg ctttttcgaa 120  
gcacgggcat accaatctag ttct 144

<210> 67  
<211> 145  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_206502\_14

<400> 67

agaagaagac gacgacatcg aagagccaga agacgaagac gaagaagagg aggaggagga 60  
cgacgacgac gacgacgtcg ttctgcagga gcaatcccca ttgtcgcggc tgcgcgagca 120  
gcgttcgaag ctggaaaccc tgtcc 145

<210> 68  
<211> 145  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_221223\_13

<400> 68

ccagagtctt gtaagaaagc catcaattac tgtcagttat acagcctaaa aaataagtaa 60  
aataaaatta ctcttgtaac atgcgaggaa gagagagaga gattggcgcc aaagtttggt 120  
agaaagaatg gacatgtgtc agctg 145

<210> 69  
<211> 146  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_169084\_14

<400> 69

tttgcttgaa taaatgtgca cagaattaca tttttttggt ttgttttttc tactaacaag 60  
tagtgactag tgagagagag tgcttataga tgttctcttt tgacaatgta cagagttaaa 120  
aaaaattcag aaggagcaac ctttgc 146

<210> 70  
<211> 292  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_94891\_14

<400> 70

catcaacaaa tcacacacac acacaaacac aaagtgatat atatctccgg agagaagaag 60  
 aaacaaagag attcattttt agttactatt atttttatta taaattaaat aataataata 120  
 acaatgcctt cttctcttca gttggagggtg ctgtagtgct tgaaacagtt gcatcgtttg 180  
 gccttatgtt cttcttcttc atatggtgtg ttaaaatgga tgttgccaca ttgatgaaga 240  
 ctgaaaagct ggccatcact gttggtatth ctgtgttcgc atttacattg gt 292

<210> 71

<211> 147

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_281852\_61

<400> 71

aaccagagga aacagggagt catttcagat aacataatgc agttcatatt taccaatata 60  
 tatatatata tatatatata tatatatata tatatatata tatatatata tatataccac 120  
 aaacgacgga ggattaatga aagactg 147

<210> 72

<211> 147

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_46583\_12

<400> 72

gtaacaaatt ctgaaccctg catgttcatt ctctctctct cacgctcgca acccgcgcg 60  
 gcacctacac ttcttttatg tcatcacgtg ctctctctca ctctccctct ctctcactac 120  
 aaaaaccatt cttcaacttg caacaca 147

<210> 73

<211> 148

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_306835\_13

<400> 73

agtcctccag atgatcaatt ctgctcatag gcttttattg cttgcattct atgtccattt 60

caaatagtaa gtcactatat atgacgtggt tggtttcacg tctttacagc gtgcgtgcgt 120

gttttagtttc acgtcttgga tgtgattt 148

<210> 74

<211> 149

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_85471\_12

<400> 74

cgtggccact tgatctataa gagagttcta attgaccaat taattagtga aaacatataa 60

aaaggaaagg aaacatttgt ttccttaaga atgaagaaac caaaaagaag taaagaagaa 120

gaagcaaggg aaagcaaaga agctaatat 149

<210> 75

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_257208\_12

<400> 75

ccatgaatga aactcaccaa actgaagaga ggcagagtca gtgacatgat gagggagtat 60

ttgtataggc actgcaaagg aagaagaaga atgatcactg cattgagccc agctgctggt 120

gcccatgtgc cagccagaat catagtaatt 150

<210> 76

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150390\_17

<400> 76

ttacgcactc agatttggat ttgattacta ctgcattaat atataaataa ttaattaatt 60

gcttgcacgc atgcatgcat ttgtattaac tagggctgga tagctagctt aggcggcctc 120

tactatcatg gtgattaaac ttcacacct 150

<210> 77

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_34697\_75

<400> 77

gcatgctctt aggtgattgc agagcatcct ttggttatat atatatatat atatatatat 60  
 atatatatat atatatatat atatatatat atatatatat atatatatat ttgtagaaac 120  
 atgaaggata cattcaactg ctttcatgaa 150

<210> 78

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150374\_13

<400> 78

ttacgcactc agatttggat ttgattacta ctgcattaat atataaataa ttaattaatt 60  
 gcttgcattgc atgcatgcat ttgtattaac tagggctgga tagctagctt aggcggcctc 120  
 tactatcatg gtgattaaac ttcacaccct 150

<210> 79

<211> 151

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_40513\_22

<400> 79

attctgaaat tgggtgaagg ttctgaatcc agcaaaacac atcaagaaag ttgttagcca 60  
 tggatcgaat gaagcaactt aattaatata actctctctc tctctatctc tctaattcgg 120  
 ttgcattcag gtgtggcttc acatttatatt g 151

<210> 80

<211> 151

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_268602\_14

<400> 80

aacacgtctc atctcaagaa gctcatgctt ttcaatctgc attccagata ataataataa 60  
 tctatcgggtt tcctataatt aactgaaaaa tagtcaacat gaagaatgaa tgcagccaac 120  
 cttctgtgct aggcctatatt ggtcgaagtt a 151

<210> 81  
 <211> 152  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_25357\_13

<400> 81

actttctccca cacttttcct ttctctttcc ctatcgccaa cggttctcct atcacgcgctg 60  
 cgtcgtaaat cctcgaagtt atcacttcct cctcctcctt cttcttcggc ggctcctccg 120  
 gcttcggcgc cgaagccaga ggagattccg ct 152

<210> 82  
 <211> 152  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_137548\_13

<400> 82

gtatgaaccc taaagctggc ttcgagggca gcaaacctcc agcaagaaga agaagacaca 60  
 gaggtaagaa aagggaata tcattttctc attcatcccc ttgcttggtta tttacatgga 120  
 tatatatagc attcctctta acaaattctgt gc 152

<210> 83  
 <211> 152  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_139131\_13

<400> 83

gtatgaaccc taaagctggc ttcgagggca gcaaacctcc agcaagaaga agaagacaca 60  
 gaggtaagaa aagggaata tcattttctc attcatcccc ttgcttggtta tttacatgga 120  
 tatatatagc attcctctta acaaattctgt gc 152

<210> 84  
 <211> 153  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_203855\_12

<400> 84

ttgttgctcaa gagaagggaa gctcttttaa gacagaggcc tcttggaagc ttttgcttcc 60  
 tgatgctgca ggagattcct tctaaattag ctaactgaat accactaaca acaacaacga 120  
 gatgcctaaa acaacacaga tgtgagcaca tga 153

<210> 85  
 <211> 153  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_199049\_15

<400> 85

ggcaaatcac atgtacataa gggagataaa agaatgcgat tttttctttt cttttcctgc 60  
 ggtgcttcgt ttggttatgg tttatgaaat tataactaaca aaaaaaagtt tcacatcagt 120  
 taatttcatt tgctcagtg gtttatttgg tga 153

<210> 86  
 <211> 154  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_320907\_12

<400> 86

gattcgccgg aaattctctc ctccgccgcc gccgtcctcg tcaccaccgc cgaaaaagaa 60  
 ggggaacctt cgcgcgcggt cggataagtt gcagaggaaa atcgcggggc cgcgggggcg 120  
 gagagggcgg aggatggcga gcttaatatc ggag 154

<210> 87  
 <211> 154  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_16407\_17

<400> 87

cacactctca cagcaacttc tcgatctgat tactctgaac tttgtctcca aatgggcatc 60  
 cattttttca ggtaagtcaa accaaaccaa accatgcata aatacatata cacttgcacc 120  
 attttgctgg aaatcccacg tggatcagtg atat 154

<210> 88  
 <211> 154  
 <212> DNA



<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_206516\_17

<400> 88

cagaagacga agacgaagaa gaggaggagg aggacgacga cgacgacgac gtcgtttcgc 60  
aggagcaatc cccattgtcg cggctgcgcg agcagcgttc gaagctggaa accctgtccc 120  
ggcgattggc gtcggagctg gtcccaatcc gagt 154

<210> 89

<211> 155

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_264495\_13

<400> 89

agtggcataa agcaagaagt tcaccaaacg aatatttttt attctacaga aaaaaattac 60  
tattactaat actattatta ttatttgact ccattaaaga cccgagtcaa ataattccta 120  
ccatctaaaa ttcagtatgc attcccttga atctc 155

<210> 90

<211> 156

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_156785\_13

<400> 90

atctagtgcc tccacgcac tctaccctca aatcttcacc acacaacact acctcaatta 60  
ctcaactaaa gcttcattca ttcatcgtgt cgtgttggtg tctttgcaac catgcttctt 120  
agaacagcgt cctctttctc tctcttcaac gccaac 156

<210> 91

<211> 156

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_187129\_12

<400> 91

tgattgggaa ggaaagcttc attagatgtg ataagttaaa taatttaatt gagattagtt 60  
gtaataataa taaaaatctt tagaaatgca gcttgtgatt tggaggttgt gatggatgag 120

tttcgggtacc gggtttggtc atggtgcaag ataaat 156

<210> 92  
<211> 156  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_214106\_13

<400> 92

ccatcttctt ctcaatcctc atgttgccac gtgtctcgaa tctccaccga gaccttggag 60  
gtctcgccgc cgccgcctcc cgacttcaac ttccgcccgc aaatcgccgc cctcgccgac 120  
ctccgcgaca ggctctccgc gtgctctact ttaaac 156

<210> 93  
<211> 156  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_149013\_12

<400> 93

aagctcaacg tggatgtttg ttagacatac aattacaaac actcacgtga atacacacgt 60  
taacattact ttctctttct gtagttgtgc gcatactttg actcaattca acaattatat 120  
atatataaat caaagcgaaa taaatgtcta gtgtgc 156

<210> 94  
<211> 157  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_326352\_16

<400> 94

gttgttacct tgtgtgttcg ctttgccaac gttttcaatt acttttcttt tcttttcctt 60  
ttttttaaat cactccaaat accaaacacc ctctccaatt ttgggacctc cctccataa 120  
tacaattata gtgatatgaa cttgcttcca caaccct 157

<210> 95  
<211> 157  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_278962\_12

&lt;400&gt; 95

tcgaatctat cgcggaatac tcaattcggg agagagagag aaaaaaaca gaatctagta 60

aagcatgata gttattattc tactgctact tatcacaaga tagcagggtt tgttgtagtt 120

aagtagcgaa gtggagttgc aaattgagct aaggaaa 157

&lt;210&gt; 96

&lt;211&gt; 157

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_256930\_13

&lt;400&gt; 96

tgtgacctat ctttcctcgg ttctcccttc atccttttcc aaccattaag tcaaccttat 60

atcttcctgg ataatactac tatgtatgta tgtcactcat gaaaactgaa aaagagactc 120

gtgcaataaa aattggttta cttatcaga cttggga 157

&lt;210&gt; 97

&lt;211&gt; 158

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_29646\_14

&lt;400&gt; 97

acgcaactca gatgcattaa cacaaatata cacacacaca caaataaata gagagagaca 60

tacatacata ctttaaataa atgcacagta tttattaaga gacattgatt atcttacact 120

aatacataac tatatcagtg gacgatgatc attattca 158

&lt;210&gt; 98

&lt;211&gt; 158

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_29618\_13

&lt;400&gt; 98

acgcaactca gatgcattaa cacaaatata cacacacaca caaataaata gagagagaca 60

tacatacata ctttaaataa atgcacagta tttattaaga gacattgatt atcttacact 120

aatacataac tatatcagtg gacgatgatc attattca 158

&lt;210&gt; 99

<211> 158  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_108561\_14

<400> 99

aatgttgctt gccttcacag ctaagcgagc gaggaagatt gagaataata ataataactt 60  
 tccttggtca aataggatat acattacatc aaataaacia aaagggtgtca acaaatatac 120  
 gtggctatct ttctctgggt tatgaataag gggttgga 158

<210> 100  
 <211> 158  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_143975\_14

<400> 100

cggtagctat agcgtattgc acaaaagggg gtgatcatga aatgaaatga tgcatttagc 60  
 aattgtttgg tccttgctt ttttgatga cctcggatag aagagaaaac gatcgatata 120  
 tggttatgac ctgtgaatgt gatactactg acgatggg 158

<210> 101  
 <211> 159  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_108431\_20

<400> 101

ccgaatgaca gagaggaaga agaaaaaat taatgatgaa aataatattt gtctttgcag 60  
 ttttattagt attattattt ttattattaa gaagtagtat atttccaagg ttgaaatgtt 120  
 tttgagcctt tgagggtcag tgggtgtggga agttgaaat 159

<210> 102  
 <211> 159  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_281764\_11

<400> 102

ttcctgggtga gtaacaagt tagggaactt tcctgcaagg ttttcacaac ataacaaaat 60

taactaaagt tacaagaaag aaacacacta taaaaattct ttcaaacaaa gcaatccact 120

atatatatat tccgtcgttt gaatagagca tgaaccaga 159

<210> 103  
<211> 160  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_130058\_15

<400> 103

agtctcgctc ctatttcgag tcctttcact accctttcaa caaagcttct tcttcgggtca 60

acaattcttc ttcttcttcg ttgcccaaca ggcgcagatt gcttgtgtgc catgacatgg 120

ctggggggcta cttggatgat aagtggattc aagggtggcac 160

<210> 104  
<211> 160  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_310590\_52

<400> 104

ttccctaata atggtggaag cagttattat gtgatgtggt taacctttca ttattattat 60

atatatatat atatatatat atatatatat atatatatat atatatatat ctttcatttt 120

ctttaaaata atgtcgtaga acaccatatt gggtttgggt 160

<210> 105  
<211> 161  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_313405\_14

<400> 105

cggatgttaa atgattgggt cgtttttcag tatcaattga cttgatgttt atttatgtta 60

ttatttattt atttgttggt aattattgac taattttcat gataatagca aaatgtccgt 120

acataattta gagaaatttc cagaaccagt ccaacataat t 161

<210> 106  
<211> 161  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_302190\_13

<400> 106

ttaacccact accaaatata ctccaaaagg aaagcgaaca tgtttttaaat ttcattctct 60  
taattaaaat ggtaaagaca tgaaatcaaa tcatgccaat aaataaataa ggtaactaga 120  
aataatttat ccctgatcg tgttcacct aaccgaactt g 161

<210> 107

<211> 161

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_225343\_17

<400> 107

cccgcaattt gttatagtgg gaaaaataa taaaataaaa taaaacgaac taggcagttg 60  
aattaaacaa gtggactctt tccaatgtag agttggaggc tgcattatct tctttgatac 120  
ccttttcaat cttccaccat gcgtttgaag tgacatttac t 161

<210> 108

<211> 162

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_208823\_14

<400> 108

tactttccaa attgatgcag accagaaatt ttaaatgaat ttatcgttat aactatatat 60  
ttgtaattaa ttaattattg tggttacttt aatttgaggg atttgattgt gtatagattt 120  
ttattcccaa atttatttcc ttgtaactcc ctatttgga ca 162

<210> 109

<211> 163

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_74285\_11

<400> 109

tgatgacaat gatgacgatt tgtgataatt gttgcaaaaa aagtgaaaag aaaataaggg 60  
gttaaagaga gagagaaaat tgtagccttt caatatTTTT ttaaatttat taaaagggaa 120  
aaaaactttt atagctagct taccaggacg ttgcagatga att 163

<210> 110  
 <211> 163  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_109052\_16

<400> 110

cacatttgat gattgattcc agttttgcac atacaatgca tacattactt tttttattat 60  
 tattattata tgctcggctc aatttggatt cggggaagta gtacatgttt gtttgagctc 120  
 gcacaaaata tattttatta gccagaaagc actgacatta tgg 163

<210> 111  
 <211> 163  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_6395\_12

<400> 111

tactactgaa ccgtggtgcc tgatagcaaa aaaattattt ttttgtgacg gtcttatcct 60  
 tgagtcgtcc ctgtaatcta gctaaagtaa atgttgcggtg cgttcgctat tatatatata 120  
 taattgacaa tattaacat taaccacaat gcatttgtat ggc 163

<210> 112  
 <211> 164  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_244905\_16

<400> 112

tgaaatccaa gtgaaagatt gttaaaaatt ttataatttc taattaatta attaatgtga 60  
 cttacatatt atattataac atatagttaa cattaattaa ttaagaatta caaaattcat 120  
 aacattaatg tctcaatcca tggacgttgg aggtaatacg cata 164

<210> 113  
 <211> 164  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_244956\_13

<400> 113

tgaaatccaa gtgaaagatt gttaaaaatt ttataatttc taattaatta attaattgtga 60  
 cttacatatt atattataac atatagttta cattaattaa ttaagaatta caaaattcat 120  
 aacattaatg tctcaatcca tggacgttgg aggtaatacg cata 164

<210> 114  
 <211> 165  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_117220\_13

<400> 114

aagagaattg gcaaagtgca gtagcggtag cgaaggtag gtgttgaaga agaagaagcg 60  
 tgaagaaagt gacgatgatg atgcgttgag ccaccattgt cgtcattgtt tgaaggggtga 120  
 aaacgcacgc ctattatttc atgctgagag tgaagaagat gggag 165

<210> 115  
 <211> 166  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_134707\_14

<400> 115

tgtacatcaa actggcaagg aagaggtgaa caacacaaaa tctagctctg aaccccatc 60  
 gaagaaataa ttttctgcag gataacttaa aagcctaaac aagaccctag caatcttctt 120  
 caaaaataaa taaataacct taacaatttc cttctgtgc aatctc 166

<210> 116  
 <211> 168  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_35078\_13

<400> 116

agcaagatca gaagtcgcaa acacacgagc agagatggca gtcggcaaag cacgttcata 60  
 acaaaaaaaaa aatgcaggta gagatgagga gagagagaga gttacagtga aaggaacgaa 120  
 tggcaggcga ggattccatg ggaagaaatg gaaatggaag aatgggag 168

<210> 117  
 <211> 168  
 <212> DNA



<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_210506\_16

<400> 117

ttgatattgt tgcaaatcac ctgaatataa tttatatttatt tatttttactc tttcaactat 60  
gtactgataa taatataatt tagagaaaca accagttgtg gttgtaaggt tggcaatggt 120  
tgacaaaatt atccaatctc ttttctgatg tggcacttac ttgacctc 168

<210> 118

<211> 169

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_116961\_26

<400> 118

atccgggaaa tgattctaaa catgaatcaa ggaagactga aatatgaaaa ttcaattaat 60  
aaaacaaatt acagaaatat atatatatat atatatatat atcctaacaa tcaaaagggt 120  
atggaaaaca gagaaacaag aagaaaagac ggaacagcgt caaataaac 169

<210> 119

<211> 169

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_51073\_13

<400> 119

caaattgccca catttctcat gtcagttact cgtattctcc cataaataaa taaggcttct 60  
tctgtctcaa tttattttac ttctaaagca acaatttctt tctttctcat tttttttgta 120  
ccctctgatac agatcgtagt ccgatacctca agccttagcc tctacacac 169

<210> 120

<211> 170

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_55291\_15

<400> 120

ccctagggac aacagggtag ctaattaatt ggtaccacaa cggggagaaa atcaaacagt 60  
ttgtggaata tacataccta gaattgaagg gctagctcaa tcaagctaaa cttgaattca 120

actatagaaa ttaaattaaa ttgaaatttg gttacacgag tcaggaccat 170

<210> 121  
 <211> 170  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_229651\_18

<400> 121

acaatcaagg aatctaagcc acacattctt taacatttat tattattatt attaagttaa 60

atttatgttt aagtgttact aaatgatgtg actgtaaatg ttccactcta tttagtaggt 120

ctcacagttt cacctaataa taaagagtgc caacattact gcaagaacag 170

<210> 122  
 <211> 171  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_303308\_19

<400> 122

caactcctct ttcaattcgc acacacccaa cccaacccaa cccttttaaat caaaacccaa 60

aacttggttc catttcatac ttcatatat atgtatatat acatacatat acacgaattg 120

aagctagcct atctagtata tatcttacc ttagacacaa caaattccac a 171

<210> 123  
 <211> 171  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_168373\_20

<400> 123

gaacaggcta tcatggctga agaaggtagg ttagttttgt actttttaag tgtgtactat 60

atatatgtct tacatgccat atcctgttag tgaaacttgt attatgtgtg ttgtgtgtgt 120

gtgtgtgtgt gcttgtgtgt gcttacacac aagcattcag catcatctga t 171

<210> 124  
 <211> 172  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_253333\_17

&lt;400&gt; 124

gtcatcaccc atataaactt gtccaataac acttgatgtg tactaaatit ttactagggtg 60  
 ttttaagtct tagtatgggt aggttaggtt aggcttgcag gacaaaactt ctatttcac 120  
 atgtattgat ttcattgatt ctagacgatt gatgttgatg gaagcgaatc tt 172

&lt;210&gt; 125

&lt;211&gt; 172

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_5791\_13

&lt;400&gt; 125

aaagagagat tagggaacca ttggatgatt gattgattat gcagttcttt agctgttctg 60  
 aagtttcatt tcactaacct atgtatcctt acatttaatg taacttttat tatgtaattt 120  
 tgttgacaga ttttataatg taaattactg acacgaaatt tctatttgga tt 172

&lt;210&gt; 126

&lt;211&gt; 173

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_206841\_19

&lt;400&gt; 126

agctgcctca caccgccaat gtcgtcgtcg acgtcgtcga gtccgccaac agaattctcg 60  
 gcgatttogg cgtttacacc aaaccgcgg tacaattttg ctctctagtg tgtgttatgt 120  
 tgagattgca ctagattgaa ttcattccaa gtgagggacc gagagatgct agt 173

&lt;210&gt; 127

&lt;211&gt; 175

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_202827\_12

&lt;400&gt; 127

agttggctca aacaaatcag attccttgga ctttcctagc aattttggtg gtggtggagg 60  
 tggaacttct tgttcctgga gtcattcatc agcaaggatt gaaaaccac caatgtcatt 120  
 tcccctaattg ctctggtggg ctttcctctg ctggtggtg gttcttctcc taaca 175

&lt;210&gt; 128

<211> 177  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_322656\_13

<400> 128

tgtcccaata tcctaggtag agccatataa tatcaacagt aaattacttc ctatattttc 60  
 aacacactta catttttagc aactataaat aaataaaatt atctaattat gttagaataa 120  
 tctcttatta tagtcaattt gtgttctcaa tgatgacaag tgaatgtgat caaaccg 177

<210> 129  
 <211> 178  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_111841\_14

<400> 129

tgcttttagct cagtaacctg cttgagaaaa ttacaacagt aaataatagt tgtcttttgg 60  
 tttaaattca tatcaccttc atattgctct ttgttttcaa ctttttccaa gtcattgttc 120  
 gtattcttgg aggagagaga gagagaatga taggatgccca gcaagataaa ctaacatg 178

<210> 130  
 <211> 179  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_192719\_13

<400> 130

gctacttctt ggcaagctct attcgaatcg accatgaagt cttttaccaa gtcttgagag 60  
 agacttgata tattatatat catcatttag tctcgccatg ggtgcatgat aggctccaaa 120  
 actcgctatt tcatcatcat cattttatac gaaaacattg accctaaagg cacaacaac 179

<210> 131  
 <211> 183  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_195630\_17

<400> 131

ttggagttga gtgttctgat ggaagagtag tggctcttgta agttctgatt ttgtgatgtt 60

tttcagaaac tgaatatatg tagatttctg ttcaatttaa tttatgtcca gaggcagaac 120  
 aaaaaaatga atgttttttc ttcttttctt ttcttttttt cattagggtc atcgtacgag 180  
 aga 183

<210> 132  
 <211> 183  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_69999\_13

<400> 132

tttccacaaa gactcctgcc cttttctatc agctaaaatt atttatgtac aaataaaaaa 60  
 ggtacaaaca caacatttat ttatgaacag ataaacgttt ttgtgagaca ttaactgaac 120  
 ctactctatc aagcttatta ttactactac tacttatctt cactccacca cactgtgtca 180  
 cta 183

<210> 133  
 <211> 184  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_11176\_13

<400> 133

cgttctcgtc gaataatacc gattcgacaa ataaaaaatg aataaattat attggcaaaa 60  
 aaaaaaatag aataaattat actttatctt ccaactatctt cttacttttt tagttttctc 120  
 tctctctcta taagttatat atttatatac aaaaagacga aattcgtaag gcaatcttat 180  
 tggt 184

<210> 134  
 <211> 185  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_228643\_13

<400> 134

gctatagcag ctaggaactg gtggaaaatg atgggtatct tggccttttt ttagtttcac 60  
 ttttgtaata gcaaacttag caataggatt atttcggttg ttgctgcttt ctcttgcttg 120  
 cctgcctata actttgcaaa gtgaccataa attttagctc cgaagttcat gctctgatga 180

tcaat 185

<210> 135  
 <211> 185  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_88478\_19

<400> 135

aagataagat gaggtgctcg tcaaaacttc tacaaaagaa ttgggtcaaaa tattttgagt 60

cagtgaatat gctagtcaca accctcttaa cttgatttta aaaataaaat aaaataaaaa 120

acctcttaac ttgcttcaaa atgaaacctc ttgcattaat ccaatcgtgc attgaatgag 180

tataa 185

<210> 136  
 <211> 186  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_108950\_13

<400> 136

agtgctagct ggacgcacaa aaaaaattaa aattaaatca tgggccaaact aaaaatgagt 60

aaactaacia tagtaatgac taatgagttg taatattaat cttcctcaaa agtaaataaa 120

taaatgagtt gtaatagtct tttgttctat tgctaattgt acacatttga tgattgattc 180

cagttt 186

<210> 137  
 <211> 186  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_121054\_14

<400> 137

ctgcatggaa agatgaagca ggtatagttt tggccttttt ggatgttagc atttttctat 60

atcgaagcat aatattctat aaatcagcat tgtttttctt atttccatt atttgtcag 120

tgtcttaccg ttacatatt tgattattta tttattttgc cttatagtct gccagggaga 180

aagcac 186

<210> 138  
 <211> 187  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_188337\_14

<400> 138

cacgtaagac caagacctaa caggaatctt tctttaaaaa tcaaaagtgt catgaacacg 60  
 agcaaaaggc caacagctac gtacgtacat ggtagttcat attaacaaat tatactacca 120  
 tcattctggt ggaaaaataa aataaaaatg aaggaaaata aatacgaaga agatgcacag 180  
 tcttgat 187

<210> 139  
 <211> 189  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_255944\_21

<400> 139

taactttgcc ttaattgggt gcacaaaact aatatttcat gattttatct tcctaattggg 60  
 gaatctatat atatatatat atatattgaa aataaagcaa ataattgccc catactgcaa 120  
 tgaatagtgg ggaaaaaat attttttgca ataataaat tactgtaggc agtgagaagg 180  
 caagaagat 189

<210> 140  
 <211> 190  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_219518\_14

<400> 140

acgaaatgct catgatcttc tttcacaatg tgatataaga cttcctgagg tatatatgta 60  
 ttctaattgtg ttttatgcat attgatttgt tttcatgtgg ttgggttggg ttcattttca 120  
 tattatacta gtttgcttat tctaggtact ttcaattatt ttatgttacg ctttctctct 180  
 cctgcagatt 190

<210> 141  
 <211> 191  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_235601\_15

<400> 141

acactcagtc atagccaagc ctaccttgac attctcataa aaactaacca aaagaagaag 60  
 aaaaagaaat agtccttgaa atttttcttt tcttattgac caaaaagaaa acaacgaaaa 120  
 taataataat aattattatt attaggaaat aaaagaggaa aatcatactt accttgctct 180  
 cgtccaactc a 191

<210> 142

<211> 192

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_301529\_13

<400> 142

ttagtttaca ctgccggatc acgttcctct gtatttattt attttttctt ttaaaaccat 60  
 cgaatTTTTT ttagaatttt ttaattatgt tgtgaattgg taatatttgg ttattaaaat 120  
 attttaaatt atgaaaatca atattgtatt attttgattt atgttgatga tttccaatgg 180  
 attagactgc tc 192

<210> 143

<211> 195

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_94795\_14

<400> 143

ccgtctccaa caccctctca tatatatgtt tttgcttatt attcaacatc atcaacaaat 60  
 cacacacaca cacaacaca aagtgatata tatctccgga gagaagaaga aacaaagaga 120  
 ttcattttta gttactatta tttttattat aaattaaata ataataataa caatgccttc 180  
 ttctcttcag ttgga 195

<210> 144

<211> 195

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_46703\_23

<400> 144



aaaccattct tcaacttgca acacacgcac acacacacac tcacacacac tgtttttttg 60  
 ttccactaaa tcaaaacctc ttatctctta ctctcattac attcattctt ttgattttcg 120  
 ttatggtagt agcagtggag aaaaccaacc tcacttcaca atcacaatgc ttcaaccgtg 180  
 tttctgacaa gaaga 195

<210> 145  
 <211> 200  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_59616\_14

<400> 145

tcattgtaac atggaggcaa ctatctaaaa aagaattgag attattttaa aactaataag 60  
 tgattgtgat agttgtgatt aattaattaa tactattgaa gcaagagac aatatatata 120  
 gaaattgtgg ttttctgttg ttttaatttg cttttggaca aagattaaac ggtaaagtg 180  
 atgatggtga tgatttaggg 200

<210> 146  
 <211> 206  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_296933\_15

<400> 146

ttagtgga aa caagcactct ctcctttttc ttttcttttc atcattggat caactttata 60  
 tttttgtgct agtgctctag tgtcactctg ctacttttga tgacactttg tagtgtttca 120  
 tattatagtt ctgttttgta attaagtctt ctttttcctt agttattgtg cttgttttaa 180  
 atacatttgg tggcaagagc atagaa 206

<210> 147  
 <211> 212  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_192428\_17

<400> 147

ataacagcga agcaatccat taaccaatat atatatatat atagacacac acattagtca 60  
 catgccaaat agtgggcaaa tctcactcat gcaaaaactt caaacagtga aacaatttga 120

tttttgtttt ccttttggaa tcacgacata ttattacaag acaaatacat tataacttat 180  
tagaagtgct acttcttggc aagctctatt cg 212

<210> 148  
<211> 213  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_191490\_14

<400> 148

gcataatata ttgtgtcttc atccattaat ttttcaaact tactaaaagg ggagtcaatc 60  
atattcatga cagatatttt ggcaaaataa aatgctattg cagaaaagac tatgcaagaa 120  
gaaagtgata actaattttt ctctctaaga ctgttggaaa aataaaataa aaatgaagga 180  
aaataaatac gaagaagatg cacagtcttg aat 213

<210> 149  
<211> 221  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_201115\_11

<400> 149

tctcattgat ccttgccat ccataataaa ttgattttac tgtttctact tttttaata 60  
tttaagtagt taaactcgac aaatatttgg ttcgttagac attaatgtga aaagacaaac 120  
gatatatata tacataaaaa acaatatatt ttttgttcca tcattttgct tgcattgattt 180  
atattatttta cgaattggac gatggtatta gtagttgtgc a 221

<210> 150  
<211> 221  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_72882\_15

<400> 150

tgatcaccac agtaatatca atcacaatag tcaaaataat aataataatg accttgatgt 60  
gaaaactgct aaagtgaatt ttatataagg aaatcattct catatagaaa tgataaaatt 120  
acttattatg agaatgaaaa caataaatc ttatttgaat ggtagattt aaaaaatata 180  
tcacttctta ttaagtgggc atgtgtgaac attaaattac c 221

<210> 151  
 <211> 222  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_69514\_13

<400> 151

aaactttgca tcacattggt aatcttttac attaatTTaa aatataattc acatatttta 60  
 tttttttattt attatgaatt ttaattataa tacatattca aaattattta tttattataa 120  
 atttttagtta aataaaataa acattttattt ttcaaattct acaagctaata aaactagtat 180  
 tactaaatgc atagagtatg agcaaattcg tgtaggtgga tt 222

<210> 152  
 <211> 227  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_37699\_47

<400> 152

gtggaatcaa gtgagggaga aactcatttt tcaatttaac tttaaaaacc aaaactaaaa 60  
 aacttacaac tatacattgt attaattagc atgtgtttta tatatatata tatatatata 120  
 tatatatata tatatatata tatatttgag tatggaagga gtactctatt caatgagatg 180  
 aatatgtgtt aacaaaaaga ttgattaggc gattaagaaa gaagaga 227

<210> 153  
 <211> 228  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_11301\_29

<400> 153

ccatttatac acacacacac acacacatat atatatatat atatatatat atatattatt 60  
 acttggttaa taaaatcaga aaaatgttgt aatcactttc aaaactgtag ttaataaacc 120  
 ttaactaaat caagcaaaaa caatggataa gatggaagtt tagtgatata aaaatatata 180  
 caggatatgt gagaataaaa aagttgagga agtgtgaaat ctacgtga 228

<210> 154  
 <211> 236

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_141875\_12

&lt;400&gt; 154

gctcatgatt cgggccatat ttttaatttag aaaatgaaaa tatttttttaa tataatcttg 60  
 ttttttcata aattgttatg tttatctttt gagaaaaata ttaaagcaac tttttaagtt 120  
 tttgttttta attagaaaag catttaatta ttattatttt taacatatgt ttaattgaaa 180  
 aaatatTTTT gccattgggtc tgatttttcta cactactcaa cacaacaatt tgctca 236

&lt;210&gt; 155

&lt;211&gt; 238

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_98090\_18

&lt;400&gt; 155

aaacacacac tgaacttggt cctaaattat attgagtaat taactaccaa agttatatat 60  
 atatatatat aatattagtc atctttcaaa agtaaattat atatattgat taaccatttg 120  
 atattttctg agcgtggaaa tcggtgaaac ggtgggcagt ggcttttaca agttgctctt 180  
 ttttggtata aaaatttgca agttgctctg aagcttctgc ggattgtact gcatatgt 238

&lt;210&gt; 156

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3\_\_43298\_35

&lt;400&gt; 156

tggttccata agactctcga acaaaattac ttccaataaa atatacatgt gggtttataaa 60  
 aaacaattcc atcaaaattt tccaaaaata atacaaaaag gatacaataa ttttttttaa 120  
 aaaaataatt catttatatt gaatacatga cttttatata tatatatata tatatatata 180  
 tatatatatc aaccgggaca tagtaattca agactactta atgttggttca cccgtgatac 240  
 atgt 244

&lt;210&gt; 157

&lt;211&gt; 248

&lt;212&gt; DNA

&lt;213&gt; Glycine max

<223> Seq ID: 240017\_region\_G3\_\_262094\_11

<400> 157

```

ggatccaacc gactagatca gtctaatttc aataactatg gtcttgtgta ttagaatcga    60
attcaaaata ttttagttat ggaacaaaac tatatatata tatatgtgtg tgtgtgatta   120
tattactttt ttaactaaat ttaaattata gagatgattt ataattatac atacaagtta   180
tggttatatga agaaaaaata aaaatttagg gggacaattg ccccttcatt cacaaagtgt   240
cattagaa                                         248

```

<210> 158

<211> 248

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_262079\_15

<400> 158

```

ggatccaacc gactagatca gtctaatttc aataactatg gtcttgtgta ttagaatcga    60
attcaaaata ttttagttat ggaacaaaac tatatatata tatatgtgtg tgtgtgatta   120
tattactttt ttaactaaat ttaaattata gagatgattt ataattatac atacaagtta   180
tggttatatga agaaaaaata aaaatttagg gggacaattg ccccttcatt cacaaagtgt   240
cattagaa                                         248

```

<210> 159

<211> 263

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_59090\_12

<400> 159

```

tctcatttat ctatctocca aggtgtgtac attccattag aatgtgaaaa tgaaaaacat    60
tcacaagcat aatgtaaaaa aaataatatt atttctcata accctatata tatatacacg   120
ccacataata cgtacgaacg taagtgatac tatcatgaaa gttcttgaat ggctttcttt   180
tcagggtgaa tacatatatt aatggatagt ggtttttggt ggtcattggt tcttattatt   240
atgtccttag gcacggtggt agg                                         263

```

<210> 160

<211> 265

<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_245723\_13

<400> 160

```
aacgttgatg tctactgctc ccaatccaac actttactct tcttcctttt tttcttttct 60
cctcttcttt ttattctttg aaaactacta aattcaaagc aaatcttaat tagaaagcaa 120
aaaagaaaga catagggttaa tgatattttt gctctctcaa ttttcacact aaacttttta 180
gttccataat caatatctaa aaacacgatt aagaagaaga aaaataaata aatagcaagc 240
aaacaaacaa ttattatcca cgcgcg 265
```

<210> 161  
<211> 266  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_194628\_54

<400> 161

```
gattaggcac ccataatata aatccttttt tcactatatg aaaaatttat atatatatat 60
atatatatat atatataata atatatatat atatatatat aattaatttt tacaataatt 120
attttaaata ttatacgtat tacaatatct cttactttta cattgtaaaa cattttacaa 180
tgaaaaaact cctagattct ataaatatat tcttttagag ttacaatttt attacacggc 240
aactgacgtg tcggagttgg taacat 266
```

<210> 162  
<211> 268  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_4566\_16

<400> 162

```
ccaaacacct cctcaattgt agacctgtat ttcaaataat aactatatga aacttcaatt 60
ctaattgaaa aataacaaaa caatacttat gaattatatg taagtgttgt cctaaactaa 120
actaaaccaa tcaacaaaga aaataactca aattctaatt gaaacaaatg aaaagatcat 180
ttcactgttc tagataaatt ttatgatata taatgtaaaa gtgaattaat acctaaatta 240
agatagtaca caggcaaact tcaagaaa 268
```

<210> 163  
 <211> 274  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_96209\_14

<400> 163

```

ttgatgagct ggctggtag ttaaataatat atttttactt attttaatac aaatgcta 60
taacttggtg acccaacata ttatttaaga aaaataaaat aaaaaatatt tttattagaa 120
aggaaaaaat tatgtttttg ttgatttttt ataccctttt aaaatttata taataaatat 180
ttttctcatt taatttttta acatgtgcta agaacattta tgagtaatat ttttatttgt 240
cataatttga agagggagcg aaagcctaca ttac 274

```

<210> 164  
 <211> 274  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_248715\_17

<400> 164

```

agcaaatgct ttaattacgc tgaaaaagta tccttttctt tttttttgaa attattcaat 60
gaattaaata tcacagtga atttaaatta aattaaattg ataacatatg tttttatttt 120
ctaatttaaa aaaaactgtc aaaaaaaatt cttttttata taaggatgat gttaatttaa 180
tttttttttg agttgttaat cttacaata cgagtagcta taatagacag cgatatcgag 240
ttgttaatac gagtagcaag caataccaca agaa 274

```

<210> 165  
 <211> 280  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_71410\_40

<400> 165

```

gagtccttca aattggcgct ttttttctcg ttttggttcc cagtacttaa gtcataataa 60
taataataat aataataata ataataataa taaaagttta ggaagaaaaa tgagaaaact 120
aattagtttc ggggttttatt taaggttttt ttagtttcag aaactaaaat gacatataga 180
tacaaattta aagattaaat tcgtcattta ctcatTTTTT attagacaaa atttaggttt 240
aagcatgcat accttttggt tcttgaatct agccaaactt 280

```

<210> 166  
 <211> 284  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_226519\_13

<400> 166

ataatgccca cgatccaagt gtattaatat ttaataatga tatgatatgt cactttcttac 60  
 acacacttca tacaacaaaa atcctcacca tttctttttt cattttgttt tcctttttaca 120  
 ccatatatct cacatttttt aggaggggaa ggataagggtt atatcacttt atttgtgtaa 180  
 gtaactttttt tggattaata attgattatt attattaaat aagacaacc gaatataact 240  
 ttttcattttt tgaggagca tgaaagttgg agtacggaaa tgga 284

<210> 167  
 <211> 285  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_11282\_19

<400> 167

cgaaattcgt aaggcaatct tattggtatt ataattttct ctactgatta tgtctaacca 60  
 tttatacaca cacacacaca cacatatata tatatatata tatatatata tattattact 120  
 tgttaaataa aatcagaaaa atgttgtaat cactttcaaa actgtagtta ataaacctta 180  
 actaaatcaa gcaaaaaaaa tggataagat ggaagtttag tgatacaaaa atatatacag 240  
 gtatagtgag aataaaaaag ttgaggaagt gtgaaatcta cgtga 285

<210> 168  
 <211> 286  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_170504\_12

<400> 168

aaccaaactt ggggtgaact tgttttacta aataatttgt ttaatatattt aaaataatgt 60  
 cttaattata ttgaacaaaa aataatatta tatattaata ataataaata aatttcactt 120  
 aaaagtgatca ttaattataa atttttttta accaaagcga tatcgttttg ataagttaaa 180  
 aaaaaaacg gttaatacaa gtttttaact gatttaacga ttttaaatcg atgtaaggat 240



ccattaattt ttaggagctc ccaactggccc gatttggatt tcattt 286

<210> 169  
 <211> 287  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_40864\_14

<400> 169

ggactgattg gtacgacccat tagtttaatt agctccatgg agaaaagcaa gataaaattg 60  
 ctaattattg gttaagaaaa taattgcacc agatatatta tataaaatgt caaaaacgca 120  
 ttccgtacat tataaataat attatatacg tcatatttac atcatttttt atccttgttt 180  
 atctcaaaaa agtgtaaata tagagagagt atatatcata tcatataata tgtaagtttt 240  
 tattagttta aaaaaatagc ttgagagtaa tgtgatttgt catgtgc 287

<210> 170  
 <211> 291  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_13529\_14

<400> 170

cgtgccaatc atcgatacag tacaaataat aaattaaaat gcaatttttt tcttgttctt 60  
 attttttctt atttctctta aactagatac tatcgaatcc attctatttc ttatctgttt 120  
 ccattattct acttctcact tattttcatt actttattcc tttcttttat gtttctatcc 180  
 actttattta tcacctattt ctttctttct taccgaatac taaacaagcc ttgtgatccg 240  
 aaagcccgaa acaatcattt tttatgaaac agcttacact ctgggtggtgt g 291

<210> 171  
 <211> 291  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_22858\_14

<400> 171

tcaattaaag ggataaggac ccatttattt aagcttttaa aaaaatattt ttttttacat 60  
 atttatgtaa agttatttta tttggttaca ataattaaaa aatgtacttt atattataaa 120  
 aagtagttat aattttgact ttttttcagc tgctactcaa agtagcttct gaaaataatc 180

atatagatag atagattctg attttttttc taaaaaaaaa cttaaacaaa cacactaaga 240  
 aatttttagaa gtgatttttc atgaaaaaag ttgaaacaaa tggggtctaa a 291

<210> 172  
 <211> 292  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_309211\_13

<400> 172

aaagttagaat ggtttgacag agataaaatg agggggattg gaataaaaaa gttatgaggt 60  
 tcattattaa ttccttatca attcatcaca tatttctttt cacctattta tctatttctt 120  
 atttatttat tttcattatt cctaaactaa ataactttgt ttctatttcta cttcttatat 180  
 atttctattc acctttttta atttctagtt atcatatctt gtacttcttt taatttttct 240  
 tccaacccaaa catattttaga aactactctt gggataatca gcagtagtgt tt 292

<210> 173  
 <211> 293  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_55568\_26

<400> 173

aggcatagaa gcactaatgg tgacacacac tagtataaaa atactttttaa tatcagttat 60  
 ttttagatttt tttgtttgtg taagtcaatc aatttttaaaa gttacttcta aatcaacttt 120  
 aacaaaaact aatgtagaaa tgatctagaa aacttttttt ttaagttcta actctttttc 180  
 atcaatgtta tacatatata tatatatata tatatatatc ccaaaataac caatcaaata 240  
 aactacttag tttacttata tgttaaatca tcgacctatt acaagagagg agg 293

<210> 174  
 <211> 300  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_73238\_16

<400> 174

tggtcatgtg tgaacattaa attaccttta atctttatca taattactct tttcattctt 60  
 aaattaagat tttttttcta atttctagat atattaatta tttttttctt aaatattctt 120

acttaattat tttctcatca aatattaatg agatgaatag agaaataaga aaagaataat 180  
 ttttgaatga taatataatt aattaattaa taaatttaatt gtgattaatt aaattaatta 240  
 tttttcttaa gacacataaa ttagttgaaa ggtaattgta ataagggaca gacggagtga 300

<210> 175  
 <211> 300  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_52488\_19

<400> 175

atgtgcattg gatgttctac catagtacat tgctttatgt gaaagtcttt taattattca 60  
 atattgacat gttcttatat atatatatat atatgaggga ttgtattatc tctgaaaaaa 120  
 gattttatca taaaatcata atgatttctc ataatgtatc tttacatttt aaagtttagat 180  
 aaataaaatt gattttaaat tgtagatat aattaaata cataattaat atgactttta 240  
 acaaattgat atataaacac ttaaaaaaaaa gtttcatgac gtacgggtgtg tattgttggg 300

<210> 176  
 <211> 104  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_471518\_14

<400> 176

ttgcaactac ctgcaacgag gatactcaca caatgtgtag ttatagccaa gagtttttct 60  
 tttctttttt tcctattagg agaatctogc gtaattacat aatt 104

<210> 177  
 <211> 105  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_231599\_23

<400> 177

cttcaaggct ttggagaaca aacatgacaa gggaggagga ggaggaggag gagggagcgt 60  
 tgctgaatcc gacagcgact ccgaggagga ggagtaacgag gacct 105

<210> 178  
 <211> 110

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_375912\_13  
 <400> 178  
 gacgcacatctg tcacgaacga cggcctgcag cgaggagttc tcgcagagaa gacgaagctg 60  
 ctgtcgcgaa gaagaagaag gcgtcgcgag gaagaagaag gcgtaggttt 110  
 <210> 179  
 <211> 110  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_180013\_12  
 <400> 179  
 accagtactc ctggagggtc tcacccttcc aggccaagac ggccggcactg tcgcgggcaa 60  
 tagcggcggc gccgtggtcc tgggtggaga agatgttgca ggagcaccag 110  
 <210> 180  
 <211> 113  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_171606\_14  
 <400> 180  
 gcaactcgac atattctttg ggattttgat gcctatttgt tacgaagtct atttaataata 60  
 gagtttagtt tagttatcaa ttgcagggac ttcttcagtc ccacattgga aag 113  
 <210> 181  
 <211> 114  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_416256\_13  
 <400> 181  
 aacaattgca tccggtcatt ctaatgatat attatttcat cccacatcct cccactaaa 60  
 caaccttcta tgttgatctc tctctctctg tctggcctct tgagtgtgag aatt 114  
 <210> 182  
 <211> 123  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_231395\_15

<400> 182

gtccttcccg cactaattta tcgaaaatct cccttcccag aaattagggt ttagtatttc 60  
 tttctttctt tatttatcag cgattcgtgg caatttttcg aaggtagggg ttgatgggtg 120  
 atc 123

<210> 183

<211> 125

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_5502\_47

<400> 183

cagcaagagt tgacgaatga tgaacatgct tcaaatggag ttatatatat atatatatat 60  
 atatatatat atatatatat atatatatgg tcttgcacga ggtatgaggt tgcgggtgtt 120  
 aaagc 125

<210> 184

<211> 125

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_93061\_14

<400> 184

acagcatcag aactcagaag cattggttgc atcagagttt tgttatggtg tatttagaaa 60  
 aatctttctt gaaaaaataa aataaaacgg tatttcgcca acaggtcagc aacaacgtta 120  
 gcctc 125

<210> 185

<211> 127

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_111684\_19

<400> 185

cttctccata acacttccca ccaaccaag ttcaacacct ctctctctct ctctctcaca 60  
 caaacacttc tcccaacct aatgtctctc cccaaaacc tactttctct ctctctctct 120  
 ctcacga 127

<210> 186  
 <211> 128  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_69328\_14

<400> 186

ctcctcagcc aggttacgct tattgacccc cagcgcgcc agggtcttaa agttgtcccc 60  
 gttgctttga acaaggctct tcctctctct ctctctgttt ccgttcttta tttctctctc 120  
 gcgtttgg 128

<210> 187  
 <211> 130  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_36529\_17

<400> 187

tcagagactt ctttgcttgg atgaaattgc aggttcactt cctctctctc tctctctctc 60  
 tacttcaatc ttgtgttgcg tagaatatgg ttgtgtttat aaaaattggt tgcattcgtt 120  
 cctgtagttg 130

<210> 188  
 <211> 132  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_139128\_12

<400> 188

cagttcggcg atatctgatt ctaccttcac tgggtgaaga tactaaacag ccactttgga 60  
 ttttacttgc acgcatatgc gcatgcacac acacacataa caaacactga caaggttcaa 120  
 gaacttcact gg 132

<210> 189  
 <211> 132  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_495674\_13

<400> 189

aagaatccag gaccatgacc ctattaatga aaaaacctgg gaaaaataaa taatatataa 60  
 gaatatatgt aagctccagg tccaaacaaa caaaccaata ataagttaat aacatcagag 120  
 aatgaccgca aa 132

<210> 190  
 <211> 132  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187577\_13

<400> 190

aaacgaacac atacgcactc acatttccat tccacctcaa caaacacaac aacactctct 60  
 cttctcgctc ttggcttttc gctcttcaact cactctcatt cattcatttc caccgttcat 120  
 ggatccagta ag 132

<210> 191  
 <211> 134  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453036\_14

<400> 191

caacaatccg tgttgataag agcaaaatat ccttttatta tttatttatt tgatagtcaa 60  
 tatacatatt ttgcctcgca ccattaaag agttggggtc ataatgtaat ttcgggacta 120  
 gaagtgcctt aggg 134

<210> 192  
 <211> 134  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_374041\_13

<400> 192

aatgcaaagt acaaagcac cctgtctaag tgcaatacga ttaactctta aggtaacgat 60  
 agcttcttga tagcatgtta ttattattat gtaataataa catgcttttt ggtcattatt 120  
 catggtggaa caaa 134

<210> 193  
 <211> 136

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_3412\_11  
 <400> 193  
 aaacactcca atgccaccat ctcaacacccc ttttctgccg ccatctccac aacgcaaaat 60  
 cagttcaggg attcaaaaaa aaaaaaaaaa accagagaga gagaaagtga aaaagggtgtt 120  
 ggcttttggtt aaggtt 136

<210> 194  
 <211> 137  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_276495\_28  
 <400> 194  
 ctttcaagcc gcagggttag atacgtgtct tagttattat tattattatt attattatta 60  
 tatgtcgaag tcatacttag ttatgatagc tagctaactc ttttattaac tataataatt 120  
 ggctacacgt tgcagct 137

<210> 195  
 <211> 139  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_151839\_17  
 <400> 195  
 ccgcaatggt atctctctca gacttgggaa caaacacagg cttcaccata gccactcccg 60  
 tatattcctc atcagagtca gtctcatact cagattcctc ctctctctcc tctttctctt 120  
 cctctctctc ctcttctg 139

<210> 196  
 <211> 140  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_292912\_12  
 <400> 196  
 atatgtttgc gtttctgtgc ttgtgtgttg tccgtaaata tatatatatc tcatcattat 60  
 tgttagtggt attggcatg tgtttctttt tctttatatt ttttctcact ttctatgctc 120



tttctctcta ttcctaaggg 140

<210> 197  
 <211> 141  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_104560\_12

<400> 197

aagagacaaa tggaggaaat tgcacgtggg ttattagatt gtggacgtcc atttttgtgg 60  
 gtcgttagag aaaaggtaat taatggaaaa aaagaagagg aggaggagct ttgttgtttc 120  
 agagaggaat tggagaagtg g 141

<210> 198  
 <211> 141  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_65193\_11

<400> 198

tagtggaatg gaagcagaac agagggaggg ttggtgtatg tgtgtgtgtt agagtaagat 60  
 aaacagagaa gctgcagaga aagaagaggg taattacaat ggaagtggac tagtacactc 120  
 ctggtttgga agaacagcat a 141

<210> 199  
 <211> 284  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_110573\_70

<400> 199

cacattgaaa taaacatgta cgacacacat atatacatat atatatatat atatatatat 60  
 atatatatat atatatatat atatatatat atatatatat atatatatat tttggcagca 120  
 cacataaata ttatatccag cgtcagcggt atcctcttct tcaaagggat tgacttcccg 180  
 ctccctgcca cgatcccatc caccactttt gtttccccat ccacctgtac gtccaccacc 240  
 accaccatac ccaggacgat aatcatttct ggggtgcagca taac 284

<210> 200  
 <211> 144

<212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_65117\_12

<400> 200

tgcaagtgtga gttcttcttt gatcctgggt atccattgac aatgaaagag agtaagaaaa 60  
 tccaacaagt gaaaaaccca gaggaagaag aagaatggag aggccagaaa aacaaaaact 120  
 ttagtggaat ggaagcagaa caga 144

<210> 201  
 <211> 144  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_490837\_16

<400> 201

agagaacgaa cggtagcatt ctcaagtcaa ggtgaggagt atggacgata cataaatgtt 60  
 agttgcgaac aactctctag tctagtctag tacatcatgt ttaggttgga ttagtattta 120  
 ggaaagtcaa cacacaatgc atgt 144

<210> 202  
 <211> 145  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_107448\_11

<400> 202

tcagaaagtt tcctacttg attgagggtg gttttttctt aatactagct gagtgaagaa 60  
 aggatatata tataatccac cggcagattt gggttctggt aagtgatcag ttatttctaa 120  
 atcaaaccag aaattgatcg aagga 145

<210> 203  
 <211> 146  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_331\_23

<400> 203

ccattgtcca tcctctctaa tgtttctttt accctaaact acagcttact accaaaaata 60  
 aataaataaa taaataaaac tgtaagtata gcataaccgc agacaaaatg ctatagatag 120

ttaaatccaa cactggacat gtgaaa 146

<210> 204

<211> 146

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_193470\_13

<400> 204

taggcatagc ttaaggcatg gtattaatta ttattattaa tatgtggcag actagagtgg 60

tagatatctt acttggttga gttgatgtaa ttaaagacag cactaccatc agtaaaattg 120

atatgagaag caggaaggac atgagg 146

<210> 205

<211> 146

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_183305\_14

<400> 205

ggagattaat ttgatgaacc gacaaaaaat attggtacag cataatcaca attattgaga 60

agatatTTTT attttatttt taccgaatcg tcgcacgact cggcgtgttg caaccgcatt 120

aaatctttgt gttggtctca ccctgt 146

<210> 206

<211> 147

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_55050\_14

<400> 206

tctgaccctt aataatcagg caacaaaaaa gtaaaataaa aaatagtgtt ttaaaagaaa 60

agaaaaaatc aaaagacaac aagtcaaata taggacgcat tatgcaaac gcggttctaa 120

cttctaaccg ggcaagtaga agattct 147

<210> 207

<211> 148

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_224693\_21

&lt;400&gt; 207

tgggtgctaag aaagtgtaat ttgtggactc gttagaaaaa taaataaata aataaatagt 60  
 aaataaaagg gtaggtataa ctacaactat aagggaagaa tcaaaacagt ctacttagtt 120  
 atgcggtaca ccacatgttt gaaagaaa 148

&lt;210&gt; 208

&lt;211&gt; 148

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_207216\_12

&lt;400&gt; 208

ttaactttgt tagaggaggc ggagacagag gaaagagatg tttaaatac tctttgtctt 60  
 tgtttctctc tctctccgt tgaagaccta gatgacattc gacagaggag agagggagaa 120  
 ggagaacatg aagaagacaa cgagccag 148

&lt;210&gt; 209

&lt;211&gt; 149

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_4654\_22

&lt;400&gt; 209

ctgaagaaag cattgaccaa ggaaaacgga acgaggagct ggtatatata tatatatata 60  
 tatactgagt gctgacaagg taagtttttg tctactgata ttacacatcc acaaagaata 120  
 ttatctgtga ttgtgggtta agatgggtt 149

&lt;210&gt; 210

&lt;211&gt; 149

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_408959\_13

&lt;400&gt; 210

cggttgttgg aagaagttgt tgtaggggtt tgcagactgc tgcggcggcg gcgggtgtcg 60  
 atagccgccg cggaactgga aagggtggcc gtacattcgc gggaaaaata agaagcgaag 120  
 gcggcacaag cagaccacgc taactacac 149

<210> 211  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_132288\_22

<400> 211

acaggtcac taaccaattg catgtatact acggttatgc gatcagttac atgtatacta 60  
 cagatcatgt gacattaatg accaaaaagt accatatatt attattatta ttattattgt 120  
 catacaatgg tgtccaagac ataagcaac 149

<210> 212  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292822\_20

<400> 212

gctattcaca aagcaagagc cgttattagt ctctagattc tgggttttgt tgtttctctt 60  
 tgtttaccac tctgcttctt ttcttttctt ttctctgtt ctctctcttt ctctatcagg 120  
 ttatgggtat atgtttgcgt ttctgtgct 149

<210> 213  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_311076\_12

<400> 213

tttgtacttc gcacacattt gaaggatga aagtaggtag aatattttgt cttcttcttc 60  
 tatgggcgaa acttgaaaac ttctaaaaat acaattttac cattaaatta aaatgggtgtg 120  
 cccataactca ccttgggtag gagaggaaa 149

<210> 214  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_509623\_13

<400> 214

aatgagcata gcgaagcctc ctaaagcgtt tggtttcttc accaccacca cccttctttc 60

tctctctctc tttctaaaaa ccagaaacaa caaacacaaa ccgaaaaggc gaaaggggtt 120

ttccgagtga gatctagggt ttccatcga 149

<210> 215

<211> 149

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_190404\_14

<400> 215

aatctggtcc ctcaaagaac aagtgttgca gcagtaaaac tgcatacacc ccaccccacc 60

tttacacgag aaccataaga taaaaataag gaaacaccag ggcacgcac ttttcctata 120

ctctcaccaa acttcttgca taaggga 149

<210> 216

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_164916\_15

<400> 216

aggctacggt atagaccacg ttgaagtcaa acaaaaccgc tttttctctc tctaaagtgc 60

atagcgctcag cgtagttgca aattccagggt tttctctctt tactcaattc tctctctctc 120

tctgaggttc tggaaagatc aattccattc 150

<210> 217

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_21028\_13

<400> 217

gatggataat tagtcttggc catcattaata caaacaaaca cttggctatt caattccatc 60

aaaattctga caatcttttt gtaacggtta aacctccaac tttcgagtg gtgggggctt 120

cctgatcaaa gttgcttgct caaggaata 150

<210> 218

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_208012\_17

<400> 218

gttacaacag ctacctccgc agactcaaca gttcaaact ccttaagaca tccttcatcc 60  
 tcctcctcct cctctacacc ctctccaccc accacctcct cctctcctcc gccttccacg 120  
 gccccgcatg ggagaatcag gtccgccact 150

<210> 219

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_484089\_14

<400> 219

cgatcgcatg atagagttca ccaatcgttg accccgagtc aaccacgca gtgtcatcat 60  
 catcatccaa gttgactttg actgatctga gcataaacat gtcaagaata acaaatgggg 120  
 cttctgaaac gtaggagagg ccatcgtagt 150

<210> 220

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_332780\_17

<400> 220

gttacaacag ctacctccgc agactcaaca gttcaaact ccttaagaca tccttcatcc 60  
 tcctcctcct cctctacacc ctctccaccc accacctcct cctctcctcc gccttccacg 120  
 gccccgcatg ggagaatcag gtccgccact 150

<210> 221

<211> 150

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_480137\_37

<400> 221

ttcaagggaa ggagaagaat agattttttt tataagagat gaaaaaacgt gaagaatgaa 60  
 gtttagagag tgagatacgt tagttagtta gtttagtagt tagttagtta gttaggaaat 120  
 tgagatggat taaaggaaac ttaataggga 150

<210> 222  
 <211> 151  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_441056\_14  
  
 <400> 222  
  
 ctaatttgcg aacaggccac aagtaagtag taataaaca aaaataataa ataaataaac 60  
 agttcgcttc taattcattt tcatgataaa tgcagttaca ttcattctccc ctccccaatt 120  
 ccatttcctt ccgccaagaa atttcgtaat c 151

<210> 223  
 <211> 151  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_77486\_11  
  
 <400> 223  
  
 atacccaaat cccatcttcc atttctctct tttcacaca tatatatata cccctctttt 60  
 gaacacattc cctcacatca tcacaagaag cacaatttct ctttctctct ttttttgtgt 120  
 gtccaaaatg gctcctagtt ctgctcaca c 151

<210> 224  
 <211> 151  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_272468\_11  
  
 <400> 224  
  
 attggatcca tcctataagg caggatatact ttaaattcga gtaaaatata tatatactca 60  
 caagttcaca attaattttc gtgtatatca ccagcttgca tagctgaata cgggggaaca 120  
 tgcacgttcg tgttactgat gcaacgtaca a 151

<210> 225  
 <211> 151  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_425319\_17  
  
 <400> 225



taccagtgaaggatgaggtg actgtcatgg actagaagtt tgtaaagggtg ttcctacaat 60  
 atcacatggtt tcaactcgcaa tgattgtttt attttatttt attaggcttt gatattggaa 120  
 gtttgatgg atacgccctt agtatgcttc a 151

<210> 226

<211> 151

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_413879\_31

<400> 226

gacctcagc cttagtttgc tgagagatgt ttgtgtgtgt atattatata tatatatata 60  
 tatatatata tatatgagaa ttgacagata gtacaaaaaa tagttcatga tgaaggctac 120  
 agcctagcct atggtgacag attacaggac a 151

<210> 227

<211> 152

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_80477\_64

<400> 227

ggttggcctg aataatttgc aatagttcca ttcgtacata tatatatata tatatatata 60  
 tatatatata tatatatata tatatatata tatatatata ttatataaat gctattttga 120  
 accatcttct gctatcaact atcccacttc cc 152

<210> 228

<211> 152

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_277272\_50

<400> 228

cctgatggta ctcgcttctc tctctctctc tctctctctc tctctctctc tctctctctc 60  
 tatatatata tatatatata tatatatata tatatatata tatatatatt gtctgataat 120  
 aaaaaaaaaat gttgtgcatg ttcaatgaca ga 152

<210> 229

<211> 152

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_509642\_13  
 <400> 229  
 ctaaacgctt tggtttcttc accaccacca cccttctttc tctctctctc tttctaaaaa 60  
 ccagaaacaa caaacacaaa ccgaaaaggc gaaaggggtt ttccgagtga gatctagggg 120  
 ttccatcgat tcggagagag gatattgata ga 152  
 <210> 230  
 <211> 153  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_321771\_14  
 <400> 230  
 atcaaactct ggaaacaggt tgggtggggg ggatagagat acgataagat aattttgtgt 60  
 gtgttcaca tgcgtatata agtcaacgat ctagatcaaa ccattatcat aataataata 120  
 atcaaacccc attaatcca aggtgttgct gac 153  
 <210> 231  
 <211> 153  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_26788\_12  
 <400> 231  
 gaagagacaa ttgtgaggca aatcatcatg tgaacaccta gtggaataag gcttttgttg 60  
 ttgttgaaca aatcacatga acaaaatgaa cacaaactgg aggattaatc tataatgttg 120  
 atgtgtcata agcagagaac catgattggg ctg 153  
 <210> 232  
 <211> 154  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_262706\_16  
 <400> 232  
 ttccttatca cccaacatcc aaactgggcc atctataaaa actataagct gaactgagtg 60  
 tgtgtgtgtg tgtttttatc attaactagg tgtgtttatt tatctttatc aagtgtacta 120

gaatgtacgc atttatttcc cgcactccta gtgt 154

<210> 233  
 <211> 154  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_243928\_16

<400> 233

tggcatgtga aacctaaata aacaaatata tgtattaaaa ataaaataaa atatttcgta 60  
 aaaattttaa tctggattat agtttatcaa atagatgatt atgtaagttt tccgatcccc 120  
 actctaaagt tatcttccca ggcataccct gata 154

<210> 234  
 <211> 154  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_23246\_14

<400> 234

aatcaccttt ctctgtccac ctctgccatt actcttctct tctctctccc taaagctgct 60  
 gtataattac ttgattaacc cttctcata tgccttagtt tgacccttct caactcgata 120  
 aaatacatat gattggctta caaatttgag cctt 154

<210> 235  
 <211> 155  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_165406\_12

<400> 235

ggcactgagc tgaattgtaa tgttgcatgt gtatgatgaa tgatgatgat gtgagatgga 60  
 gaaaaatgta tagggagata gagagagctt caatttgaat ctcatagagt ctatttgaag 120  
 atatatgtta cttagggtta aagagatcga caagg 155

<210> 236  
 <211> 155  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_486294\_14

<400> 236

cttatggcca tgctatacac atgctaggat tataagtata aatagtgatc tttcaggaac 60

aaagaagcca ttctacagca aaatcgctct ctctctctct ttcagcttag agttttacct 120

tatcttctat aatggatcat ggaaagcact tcagt 155

<210> 237

<211> 156

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_46754\_12

<400> 237

aatccaaagt tgtcaagatg gttccagatt tatcatgttc gttccattta tttttttact 60

atttattgtg gtttatgaat atgatggatg tggtgatgat gatgaagtgc caacatttag 120

aaacaagatt tttcaaatct aacgatccga caatga 156

<210> 238

<211> 156

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381116\_15

<400> 238

aaaggtgggt gtgcttccca tttatatata tatatacata catacatata ttctttctca 60

aaactcttct ttaatgctta aaaggttgct cttttatggt ttccagagga aagataactt 120

tgaatctgta gtaatggagc atctgagaat gaatgg 156

<210> 239

<211> 156

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350369\_11

<400> 239

aaaggttgaa gaagatgctg cgtaattcca attccagagg aggatttgga tcaggaatgg 60

tagtggcagt ggtatgtgtg tgtgtttgct tagtagcaat ggagtatgga gtaagagtga 120

cggaggggga agagtatttc aaaccgttca acgtga 156

<210> 240  
 <211> 156  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_138841\_13

<400> 240

ggtgcagctt aaacaatttc tgtcaaacg ttagtttg tgattttata tatatatatt 60  
 ggtgatgaat attcaattca atgcaggaac aggaaggat aagcctgact ttctggccac 120  
 agtggatgtg gatccaagct ctccaacgta ttcaaa 156

<210> 241  
 <211> 156  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_12158\_14

<400> 241

catacccttt cagagtcctt gtactgcaa tccaagaaaa caaaataaaa taaaaaata 60  
 tacatgtaga agagtttatt tgcattttta ttatgaaagc taactcccaa tcgagtactt 120  
 gcaattcaaa acgaaacgaa ttccatactt cctcca 156

<210> 242  
 <211> 156  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_315368\_13

<400> 242

cagtcagaga aaggaagcat gcactgcatc taccttaatc tacctaccca cacttttcta 60  
 tatatatata tccacccttc caagccactt tgcaacatcc atccaagcct tttctttcgt 120  
 agatagctac tacttcactt tcaccccttg ctccag 156

<210> 243  
 <211> 156  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_307549\_13

<400> 243

ctggagcaaa ggatgaaagt gaagtagtag ctatctacga aagaaaaggc ttggatggat 60

gttgcaaagt ggcttggaag ggtggatata tatatataga aaagtgtggg taggtagatt 120  
aaggtagatg cagtgcacgc ttcctttctc tgactg 156

<210> 244  
<211> 157  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_159857\_14

<400> 244

tcctcctcct agttgtgctt ctcttttctc tttaatgaat ttctcctat gtaaaaagca 60  
atagaaaaag aaaaccagtt ttaaaaaaat aaaataaaag aactaatttc aggtaccttc 120  
ttccattttg caattagatt gcggtcagca taccctt 157

<210> 245  
<211> 157  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_140551\_15

<400> 245

gattcctggg tcttgggaatt tcctttttaa tttctctcac ctttctata tattgtatct 60  
gtgctcatat gaaataatag agatgatata attttcatac tctactctac tcatagatat 120  
ccatactcat tttgtattgt catctgggat gcgtttg 157

<210> 246  
<211> 157  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_279869\_11

<400> 246

taatgtgcca acttctagca aggatggggc gtcattcatt gtgagggacc gaaccatgtt 60  
cttaattatt attatatata tatccatgaa atatatTTTT tttgcctcct aattaaattt 120  
tctacttcta tcataaattt ggccataagc ccagact 157

<210> 247  
<211> 158  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_78292\_35

<400> 247

caaattgatt agtttctttc cttctccata tatatatata tatatattat atatatatat 60  
atgagctaaa acagtaatac tgtagagttt ttgtatgtgt gtgtatgttt gtttttcttt 120  
taggtagttt tagcattgat tcttgatgaa agaacatg 158

<210> 248

<211> 159

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_185019\_12

<400> 248

aaccttctcg cgtagcttga gtagatctta aaattggata ttgctcaat taatacgctt 60  
ataatatagt agtagtagcc tagatctaga tgcagtttgt cccgcgttgt aattaaataa 120  
aatatcacgg aattattatg agagcattgg tgagcatga 158

<210> 249

<211> 159

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_409164\_13

<400> 249

aggagaaaca tcagcatcat tacggggttt tgtttagtag taatgtaatt gtaaatcttg 60  
tcattggcgcg gttcggcttt tcataaataa ataaaaataa agtcctcttg aaacacaact 120  
aaaaacacat ggagatcttt cttcatgcac ccacccttt 158

<210> 250

<211> 159

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_75392\_14

<400> 250

gaaggagcct catcattgac ctaaggggat gaaatcacac tctttttatg atctatcctt 60  
tgcttttcac gaaggctgcc atttgatgag gaataagtag ttttgattaa ttaattaatg 120  
gacctataca tgtgacgata tcaaccatca atgtcatcg 158

<210> 251  
 <211> 161  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_231320\_12

<400> 251

ccctaacaat catttcaacg ccttttctct ctaatcttgc aaatcttgga aattattatt 60  
 attgaattgg gtccttcccg cactaattta tcgaaaatct cccttccag aaattagggt 120  
 ttagtatttc tttctttctt tatttatcag cgattcgtgg c 161

<210> 252  
 <211> 161  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381102\_14

<400> 252

ggccactgag aaacatgttc gatatatatt atcagttgaa aaggtgggtg tgcttccat 60  
 ttatatatat atatacatc atacatacat tctttctcaa aactcttctt taatgcttaa 120  
 aaggttgttc ttttatgggt tccagaggaa agataacttt g 161

<210> 253  
 <211> 162  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_491826\_15

<400> 253

cttgtggcga tggctctctt taataaatgt gttgcagttc atgggtcaaa ccaacccaac 60  
 tttgaaggca aaggagagag agagagaggt caagggtttt cttttttccg atttgttgat 120  
 cgcagaaaat atcatccttt tgtgggattg tgaagattgg tc 162

<210> 254  
 <211> 162  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_56365\_21

<400> 254



catgttctcc acaaggaaac agagaaaaaa gagagagaga gagagagaga agaaacaaac 60  
gatgcagaga agactatacc gaaccaactt caaaatggag gaaacatcag cagggcaaaa 120  
aaaaaaaaa ctttaaagtt gtgcctgaaa ctgtagtcat gg 162

<210> 255  
<211> 162  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_372628\_15

<400> 255

aaaggaaatc tgaaatcctg tggaattagc tctacaaatg catattgatg cacatcgcaa 60  
tccaaaaaaa ttaaaaaata aaataaaatt agatgaaaaa aacaaataaa gaaagaactt 120  
aagaaatact agaagctcca tctatcagcc aagtaacaac cc 162

<210> 256  
<211> 163  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_302609\_11

<400> 256

cctaccact tcaagttcaa ctgtctatct attcatatat atataccac ccttccaaac 60  
cactttgcaa catccatcca agccttttct ttcctagcta ctacactttc attctttgct 120  
tcagaaaatt aactagctag gatggtcagt gttgaagaga tcc 163

<210> 257  
<211> 163  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_341804\_11

<400> 257

ggatctcttc aacactgacc atcctagcta gttaattttc tgaagcaaag aatgaaagtg 60  
tagtagctag gaaagaaaag gcttggatgg atgttgcaaa gtggtttgga aggggtgggta 120  
tatatatatg aatagataga cagttgaact tgaagtgggt agg 163

<210> 258  
<211> 163

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_217037\_11  
 <400> 258  
 ggatctcttc aacactgacc atcctagcta gttaatcttc tgaagcaaag aatgaaagtg 60  
 tagtagctag gaaagaaaag gcttggatgg atgttgcaaa gtggtttggg aggggtgggta 120  
 tatatatatg aatagataga cagttgaact tgaagtgggt agg 163  
 <210> 259  
 <211> 163  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_264929\_68  
 <400> 259  
 agctaaagca aaggtgggtt tgtaaaatgt caattgtttg tgcaaagcaa ttaagtcctt 60  
 ttttataata tatatatata tatatatata tatatatata tatatatata tatatatata 120  
 tatatatata tatatgataa caatgcataa agaacaatca cgc 163  
 <210> 260  
 <211> 164  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_55499\_12  
 <400> 260  
 ttgctgcaag gtttctactt aattgcccc aaacggggcg caagtactac caccctccat 60  
 ccctctccga caaccacggc caccactacc acgctgggtg caccaccacc agcgccggcg 120  
 gagtcaaaga ggccgtggcg gctaggagca ttgacataat tctt 164  
 <210> 261  
 <211> 165  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_295634\_14  
 <400> 261  
 taagttcggt ggtttgcctt gatttgaacc acaaattttt taagtataat agtaattgat 60  
 tttttaaatt ttaaaatatt attatatatg tcatgtataa taataataat ttaatatata 120

tgaatagatg aacatgttta aataaattga gtcggatttg acaaa 165

<210> 262  
 <211> 165  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_269358\_15

<400> 262

ttcatgatgg ttaggtcttg tgcagcctca ctatcaaaga agtacaccac tctaaggtag 60

tgaagcttca tggccaagtc caagccaccc gggttgtgga atacgtccga ccgggtggcc 120

cggcccggcc caactgagga tagcctcaca tcatgcacta cactc 165

<210> 263  
 <211> 165  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_457009\_24

<400> 263

tgctgccatt ggagaaagtt gttatatatga gggagtttgc tagctatagc tgtgattggt 60

ttgcttttgct tggttggtaa aggtggagag agagagagag agagagagaa gtgttttagag 120

aaaaaatgga aaattatatt atggtgagtt gagggaaatag aagcc 165

<210> 264  
 <211> 165  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_176598\_14

<400> 264

ttcactataa aggatccgtt cagcaaacac cgctataatt aatggcaatg caatgcaaga 60

ctaaacatcg aagatgagtg acacaataaa aatagttgac ccaaaaagag cacctatggt 120

ctagtgaaga atacgacttt ttcttgttgc cactctttac caaca 165

<210> 265  
 <211> 167  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_278266\_12

&lt;400&gt; 265

tcttaatggc caattgctga aagtttgaat caataattaa aagtacatac attcaaaata 60  
 ataataatta aaattacata tgatataaat gtgcattctg aattctaagg tgcaaaagaa 120  
 gaaaaaaata cttttaagct ccatgttgac ttgtttatat taatggg 167

&lt;210&gt; 266

&lt;211&gt; 169

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_391810\_12

&lt;400&gt; 266

aaggagggttg gaggaaatca tcaaggggaa tcttaggcta aacaatattt ctaaaacctt 60  
 ggtttttaac cgtgtcgaat ggcatcaagt gatccatgta gctgacctaa cttagtagga 120  
 taaagctttg ttgttggtga attgagaatc aaattgtgca cagtaagtg 169

&lt;210&gt; 267

&lt;211&gt; 169

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_269485\_15

&lt;400&gt; 267

agcctcacat catgcactac actctcttct aagaccattt ttgggtttga tcctagaaat 60  
 taaaagagag agatatcaca aggtcaagag gggttggttg tgtgttggtg ttgttgtaag 120  
 aaagtgaatg catatatata gaatgatgag tgggtgcata agtgaggga 169

&lt;210&gt; 268

&lt;211&gt; 169

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 318013\_region\_A3\_\_359247\_17

&lt;400&gt; 268

ggttgagaag gagagttaa gggttgaagg gaggaggagg aggaggggga gaggtcgtgg 60  
 gtttaaatcc tcccactaac attctaacia aaactagcca cttaaattgtc tgacaaaaaa 120  
 aatagcactt gtgatctatg atagtgtttg tatgacaatt gggagtga 169

<210> 269  
 <211> 170  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_315094\_13

<400> 269

tccatataat ggacaggata tctgaattgc aaaaaaatca tgaatctctt gtttaaaaac 60  
 agttttatatt aaaacattta ttttttattg gaatgttttc aagatgataa atgagacaaa 120  
 tcaatcaatc agacttggtta ttaaaaacaa ataatttcct cgtgacattt 170

<210> 270  
 <211> 170  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_307823\_13

<400> 270

aaatgtcacg aggaaattat ttgtttttta taccaagtct gattgattga tttgtctcat 60  
 ttatcatctt gaaaacattc caataaaaaa taaatgtttt aaataaaaact gttttttaa 120  
 aagagattca tgattttttt gcaattcaga tatcctgtcc attatatgga 170

<210> 271  
 <211> 170  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_248588\_15

<400> 271

gtctgcaagc taacagtgtc agaggatatg aatattagta ttattaacaa taataataat 60  
 aatgatgaaa cgtgtctgct aatgagattg agtgtgatct taattatttc tttgttcata 120  
 tactactggt cggcattttt tttatcgtgg taatgactaa gtgggaattc 170

<210> 272  
 <211> 171  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_252426\_85

<400> 272

tcaattcaat gataaagtcc tttggataat atatatatat atatatatat atatatatat 60

atatatatat atatatatat atatatatat atatatatat atatatatat ataagaaaac 120  
 acatitttcaa gaatttttcc actttatttc ttgttctacc taagcaaacc a 171

<210> 273  
 <211> 171  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_513314\_16

<400> 273

cttaaagtgc gttatcgtca gcgtattact attctgaggg gaaatcatga aagtcgccag 60  
 gtctgttctt ttttaaataca tgaccttcct gttagtagtg gattatagat tagattagat 120  
 ttaaaatcct attttggttaa tcggaggcat ggtcatttgg tcagtatcag t 171

<210> 274  
 <211> 172  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_68183\_14

<400> 274

caccgtgaag atgatcaaga gagagttcga gtatgttagt gcctactaaa taaaacaagg 60  
 ggacaatatt ttctatgggt tgggttgggg ttgttctcca taaagaggaa ttgttggttg 120  
 ggggtgggtgg gatttaggtt tatagggtta tccttggttg tgggctatcc ta 172

<210> 275  
 <211> 173  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_471191\_13

<400> 275

cgtcacttga cctcaacaat gtgtatgctt taaatatact tctgctagca tctgctagga 60  
 ccttctatct acacttggta ttatgtaatt ggtaggttcg atgttgacat cttttacagt 120  
 atataagtg tcatctatct atttagtcgt accataatga gattaatttg gca 173

<210> 276  
 <211> 174  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_163547\_18

<400> 276

```
tttgcaaatc atgcatccta agtttttttaa gtaaaataat aattaaataa taatttttttc 60
agtatcttaa aacatgaatc attaacttta tatatatata tatatagatt atacaaataa 120
gactttttaca aatgatgtaa aagatttttac tctgcaaata cacttgtgca ttca 174
```

<210> 277

<211> 176

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_417867\_15

<400> 277

```
gtttgggtct gaatctgaag aaacgctgcg tttcgtttcg tttgggaatg agtgacgata 60
gaatggaaga gtagtcgtag agtgtaagag aggattaagg aaatgaatga gagaaaaaag 120
caacaaaaac tccgtccagt ggggatcagg aatttcacca actacgctag attcgc 176
```

<210> 278

<211> 178

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_332465\_14

<400> 278

```
taacgctgca tgatttgagt tctgttttgt cggcggggac tagggacaaa tatatttttt 60
gttagttaat ttgtatatatt attggtgata tgtctgaagt taagttaatt ggccatgcat 120
gtgtgtgtgt gtggtagtga gaagaattga gaaaaagaat gtggtctcca aagtccaa 178
```

<210> 279

<211> 178

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_207697\_14

<400> 279

```
taacgctgca tgatttgagt tctgttttgt cggcggggac tagggacaaa tatatttttt 60
gttagttaat ttgtatatatt attggtgata tgtctgaagt taagttaatt ggccatgcat 120
gtgtgtgtgt gtggtagtga gaagaattga gaaaaagaat gtggtctcca aagtccaa 178
```

<210> 280  
 <211> 179  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_277229\_43  
  
 <400> 280  
  
 caagccaaca tacacagtgg ttctggccct gatggtactc gcttctctct ctctctctct 60  
 ctctctctct ctctctctct ctctctatat atatatatat atatatatat atatatatat 120  
 atatatatat atatattgtc tgataataaa aaaaaatggt gtgcatgttc aatgacaga 179  
  
 <210> 281  
 <211> 179  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_36366\_11  
  
 <400> 281  
  
 aattgtacgg cagacacgtc ctcgccgagg ttaagaaagt gcgctctctc tctcagagag 60  
 tcgacggcga ctacgacatg aggatggtga tggcttcggt tgtgggcaag ctcagcttca 120  
 aggagatgtg cgttgtgctc aaggagcaga aggggtggag gcaagtcaga gacttcttt 179  
  
 <210> 282  
 <211> 179  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_91970\_12  
  
 <400> 282  
  
 tctttggaca ctgtgagagg tgtttataaa tcgagagaga gagaaatatt aaagaaaaaa 60  
 aagctaataa acgtttttaa gagatatata tgggtgaggta attttgattt tgattttggt 120  
 tgtaccttag gttttttatt gaattaaata atattgttaa ggtcgaatag aatcatgga 179  
  
 <210> 283  
 <211> 180  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_211533\_11  
  
 <400> 283



gggtgtgttgg gagagtcaac agtctactta gacatgcggt acatacacca tatatttgaa 60  
 agaaaaaaaa gcgtagtcag aggaagcatg cgcgcattcta cctaccacc cttttcaatt 120  
 atgcatgtat atatatatct gagccacttt gccacattca ttcccaccct catacccttt 180

<210> 284  
 <211> 180  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_336301\_11

<400> 284

gggtgtgttgg gagagtcaac agtctactta gacatgcggt acatacacca tatatttgaa 60  
 agaaaaaaaa gcgtagtcag aggaagcatg cgcgcattcta cctaccacc cttttcaatt 120  
 atgcatgtat atatatatct gagccacttt gccacattca ttcccaccct catacccttt 180

<210> 285  
 <211> 180  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_441603\_14

<400> 285

gtggtagtcc gcaatgagac aatctggctt ggtggttcca tcacggatcg aatcatcgt 60  
 cttcgagtga gtgagtgact gatcagggtc tcaagctctt catcgacccc tcttctgatt 120  
 ttctcgggaa aatgacggga gagaaggaaa atcgcgactt ggtcttcgag aatggatgtt 180

<210> 286  
 <211> 180  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_468354\_15

<400> 286

tttcttactg cacctagtcc acgaccgtgt ctaaactgatt aaaagtgcaa aaaaaaaaaa 60  
 aagttggcct tatcaaaatt aaactatcat aatttatatta ttattacca ctaacactat 120  
 atttattata ttattacaa acttaaatac atttacggta ctttaaccga ttattcaggc 180

<210> 287  
 <211> 181

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_188983\_18  
 <400> 287  
 tgcgaattgg taacgatctt acttctcttt tatatgctac aatacaaadc ttgctttact 60  
 aactcaattg gaaacaagat ctcatcttata agattataaa aatgatttcc ttaggctagg 120  
 actatatact ctctctctct ctctctcttt cttttttatc atcgacagaac ttagatgaat 180  
 t 181

<210> 288  
 <211> 181  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_115502\_17  
 <400> 288  
 gttattggtc ggtgtacctg atcgtgagga tgattatctt atcttatttt tgggaaggga 60  
 aggactatac atttattaat tgtattatat tcttttttat ccttttttga atcagaagta 120  
 tatttatcgc atgtgccata aactttcttc tgtgcccgtt atgcatctgt gtcaactctc 180  
 c 181

<210> 289  
 <211> 182  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_163006\_13  
 <400> 289  
 tgatggtaat gaatcagatc aacgattttg ggactgttgt tgttggtcca ttttcagttt 60  
 tttattttgt ttatgactag ttgagtttgc aatcggttct tgctcgggtga ttttagaggt 120  
 tttggacatg attttagagt atgttgattt gtgtaaaact ttgttgcaat ctctgtgtgt 180  
 ta 182

<210> 290  
 <211> 183  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_119283\_14

<400> 290  
 tgaagtggag taaggtcttg tttgaaatta ttttttaatt tcaaaacttg ttttcaatat 60  
 aattttttagc tttgttatat tttaaaaata aaataaaaag aaaaaatatt tgttaaaatt 120  
 caaaaataga ttttttttaa aaaaatgttc ataaaatadc agcatctgtc aattgcatgt 180  
 tta 183

<210> 291  
 <211> 183  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_491126\_11

<400> 291  
 cctctctacc aaacacaagc agaaaatggg aggaactcga gttggcaaatt cgaacctttt 60  
 atcaacacac acacaaaaag ctgcaactaa gaaatggaga aaaagttata cgattcaaaa 120  
 gagagaaaaa aaactattat gctgataaaa aaattggagt gaattggact taccagtgga 180  
 gct 183

<210> 292  
 <211> 184  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_99512\_21

<400> 292  
 tatatcgtgc atgtttgttg gctctccttg acaagcatat ctattttaatt tatacaagta 60  
 gtaaataaaa tgataagact aaatgatgag ttacatatata ctttatttgt actcatatat 120  
 atatatatat atataattct tggatggaaa ggaccccgaa gatacttcct tgggtggtga 180  
 cttg 184

<210> 293  
 <211> 185  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_280291\_17

<400> 293  
 tgaaatccca actatagggt gacacctggc cccctactag gctcaaaca cccoctgaaa 60

taccaaaaaa caggatcacg aatgaaacat gaaggaagga aggaagggtta gaactattac 120  
gactaagggtc agacaaaata aagggttgga gaaaatccca aaatgaaatg ttgggagaaa 180  
gtccc 185

<210> 294  
<211> 185  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_138443\_19

<400> 294

tgataaagcc aaagaagtaa ctttcgttct tattttcatg tgacttgtaa caagttacaa 60  
gtcagtaata taacctataa cttactcttc atcatctgct tcttcttttg atcataatat 120  
ctgttaagtg atctttcata gagagagaga gagagagatg gagagggtgtg acaagggtgat 180  
gaacc 185

<210> 295  
<211> 185  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_115973\_14

<400> 295

ttaagcaatt gagttggatg aggtgggttag atagtcttta tgtaaatact agtagttcca 60  
atatttaaatt ccttaacatg gttggtaaag tctagataag gttttatacc tccattttgg 120  
aactaaaatc aagcctttta tccttacctt acctttcggg gaggaagcac cacttgaaca 180  
atcat 185

<210> 296  
<211> 187  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_329977\_14

<400> 296

cagagagtcg tgtttaagca tttgaaatat taaaataaaa tgtttcaaag aatagtatat 60  
tattataatt tcgttttgac ttatgaataa tgcttcaaaa cagagagttg tgtttattat 120  
tattattctt tctatttggg aatatctact aatggatcag aatagaatag atgtccttcg 180

gctttcc 187

<210> 297  
 <211> 187  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_205203\_14

<400> 297

cagagagtcg tgtttaagca ttgaaatat taaaataaaa tgtttcaaag aatagtatat 60  
 tattataatt tcgttttgac ttatgaataa tgcttcaaaa cagagagttg tgtttattat 120  
 tattattctt tctatttga aatatctact aatggatcag aatagaatag atgtccttcg 180  
 gctttcc 187

<210> 298  
 <211> 188  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_153114\_12

<400> 298

agttacaact ttcgcatcgg ttacatttta aaggttatat atatatatat atatatatat 60  
 atatatatat atatataaa taataataat ttatgaataa aaaaattata cagcaactag 120  
 ttgtcattat taataaatat agatgataat aataatattg tagcttggtc ctaaaccctc 180  
 tcctgaca 188

<210> 299  
 <211> 190  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_34581\_13

<400> 299

gtacttgatc ccagacacca ctgcgactg cgctccacc acttcctcga acgtcacttc 60  
 ctctcctcc ttctgcgct gcctcagcat ccggttatgc tcctccaccg agaaccgcc 120  
 tagatcctgc accaccgcca tcgtcaatt gagattgatt tagaacaatg gagttacgta 180  
 tacggtgtcg 190

<210> 300  
 <211> 191  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292577\_19

<400> 300

ccattgtagg aggacaagaa tcacaagatc tctctctctc tctctctttc acatgaataa 60  
 atagaagaaa gagagaacaa caatctcaat atacacaaaa ctatgtatat ctatatgtac 120  
 atataatata taatatatga ttttggggga agtacttttt tctttgtgtg ttctgtgttg 180  
 ttgtttgttg t 191

<210> 301  
 <211> 192  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_445391\_20

<400> 301

tgcatattatc attgaattag agggattatt taccctaata ataataataa taatatggta 60  
 gcggtgttgt tggcatctgc attttctacc cgagaaagca aaaagcccaa gcagtcgtct 120  
 tggtgctgcc gattgggtcaa aatatataaa tccatttggt gaaatttggt actgtattgc 180  
 attgcgtttg ct 192

<210> 302  
 <211> 192  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350540\_17

<400> 302

gggaagagta tttcaaaccg ttcaacgtga gctacgatca ccgcgctctc atcctcaacg 60  
 gcaaacgccg ctctctcatc tccgccgaa tccactatcc acgcgccact cccgaggtca 120  
 atttaattta atttaactca tcatcagtca tcaactaaaa taacactaac atgcaaccac 180  
 aatttaactc aa 192

<210> 303  
 <211> 194  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453879\_15

<400> 303

gcagcactga acatgataag agatcaaatt gttaactttt agactccata aagtactaac 60  
 tataatttaa gttatcaatg aaaagcattc ccatggctta acacaaaaat cagttcccaa 120  
 aaactagtgt cttccactga aaaacttata tttaaaaata aaataaaatt gtcctttctt 180  
 gttcttcaat tgca 194

<210> 304

<211> 194

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_201246\_13

<400> 304

tgtgtggaat gcacatttag agaagagaat aaacaaaata ttgagaatat ctaattaaga 60  
 gaatgaaaaa aaaaagaata tcactctcta agttgtctat tctaatttat attataggaa 120  
 taaataaata ataaaaaagt ccaattaaat taattcctaa taaaatttag catatcaatc 180  
 aacatcatct tgcg 194

<210> 305

<211> 194

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_326020\_13

<400> 305

tgtgtggaat gcacatttag agaagagaat aaacaaaata ttgagaatat ctaattaaga 60  
 gaatgaaaaa aaaaagaata tcactctcta agttgtctat tctaatttat attataggaa 120  
 taaataaata ataaaaaagt ccaattaaat taattcctaa taaaatttag catatcaatc 180  
 aacatcatct tgcg 194

<210> 306

<211> 194

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_503801\_14

<400> 306

atttgcattc agtgtgaaca ttgcttttgt tttgtttgtt aaatttaaac ccccttctaa 60  
 ctttcatcag ttcagaataa tgttttgccc aaaattgttg ttttcagttg atacctctcc 120  
 ctccaatgtc ttacattttt cgctgatttt attttatttc caatttgtct ttctctcagat 180  
 tatgttaagt ccca 194

<210> 307  
 <211> 199  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_302400\_52

<400> 307

tacataaaga accatgtgag gaaggcaggg aaaaaggcaa aatagagtac actttaattt 60  
 caacctgaat aggtaagaat aaataagaaa aataaaaagg atttgtgggt ttgcacaata 120  
 tatatatata tatatatata tatatatata tatatatata tatatatatg gattcaacaa 180  
 ggctatcaat caacagtca 199

<210> 308  
 <211> 200  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_448857\_15

<400> 308

atgaactgtt gttcctgtca tgtggtaagt ttaggttgat taacagtaat ggattacccc 60  
 atctgtgtat tagtatattc ttgaattgaa gtttacgtta ttaaattgaa aaataaaata 120  
 aaattctagg ctgttaaaag tattttggaa agtgttattg ttttcttttc taaattgtat 180  
 ccaaggtggt ttgagggttt 200

<210> 309  
 <211> 204  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_48364\_14

<400> 309

aacaagtcac caaggcacia ctttaccgct gcaccaggac tcgccctccg aagaaacata 60  
 tatattgatg taaataattg cagaaataaa ataccgcgaa aattatTTTT gtccaaaaat 120



acagaaaaaa aaaagaagaa gaagaaatca cttcttttttc ttaagttggt taacattttt 180

ggaattggct tggtctctgg tctt 204

<210> 310  
 <211> 205  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_251804\_48

<400> 310

tgttatcaat cgacgcaata atcaagaaaa tcaaacatgg tatcagtaat taatttttaa 60

taagattata tatatatata tatatatata tatatatata tatatatata tatagacacc 120

ccaataaaaa tcatattaaa acaattataa ttcataatat tcagaataaa taaaaatatt 180

gaaataaatg gcaacacctc atcgt 205

<210> 311  
 <211> 205  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_382583\_13

<400> 311

ccctctatca agtgtatcag cccttataaa taccatgaat gaatgaaata aagcaaggaa 60

aaagtttatc agtatattct tatagcagta gcagtagaat tagctaagta tagaagttca 120

ccctatcagt agctatgtaa cctagtactt acttacatta tccaattact tggtagtttt 180

cctgatagaa atggtgtact ttcct 205

<210> 312  
 <211> 206  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_124737\_14

<400> 312

tccaattagt tgcagaaaca agcaagcctt ccaattagtt acaacaacaa ccaaacattt 60

tcctactaag tggggtcaac tgcatatgta tttcacaata aataaataaa aaatacttac 120

caatatattt atttatttct acatttttaa tttaaaatta ggacatttgc tcaacacaaa 180

ttgtgtattg gcaccaaaga ggacta 206

<210> 313  
 <211> 206  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_124766\_13

<400> 313

tccaattagt tgcagaaaca agcaagcctt ccaattagtt acaacaacaa ccaaacattt 60  
 tcctactaag tgggggtcaac tgcatatgta tttcacaata aataaataaa aaatacttac 120  
 caatatatct atttatctct acatttttaa tttaaaatta ggacatttgc tcaacacaaa 180  
 ttgtgtattg gcaccaaaga ggacta 206

<210> 314  
 <211> 209  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_461351\_16

<400> 314

gaatggtggt aggggtgaag caactgccac cggggtgaat tgccctgcag tcagctccat 60  
 gtgagcatgc aaaggccaac cctgacttca gtgccccgta gccagcgttg ctccttgctt 120  
 cgcaccacaa tgttcatcat catcatcatg ctcccaacta ctattaacac tagagaaacc 180  
 acttttgctg cccttcaaca aattactat 209

<210> 315  
 <211> 214  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_64953\_19

<400> 315

caccttgaga aacttgaaac acttgaaaag aaaaaacaca gacacaactt caaaaccag 60  
 acaccccaga aagacaaaaa cttttcataa gaaagcacc aaagtaacaa aataatataa 120  
 taacataata atggaatatg gaaaggaaaa gagagagaag aagaggaaga agaaaggggg 180  
 gaaaagagga tgagggcagt gaccctttaa agag 214

<210> 316  
 <211> 215

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_366586\_13  
  
 <400> 316  
  
 tgtccatgca ttaaagcaaa catctagaat tagaacttca tgcactttat ctattaaatc 60  
 tttgcaaaag tatttgggag atagatagat aagatagggt tgcctgtgatt ttcagggaca 120  
 agtattccaa tagatgtcgg tagaaaaaaa tcatcaaatt gataaagaaa aatctaaaat 180  
 catacatctt agacaaataa cgcatgtttg cattc 215

<210> 317  
 <211> 217  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_46190\_15  
  
 <400> 317  
  
 caaacctcca atcactaaat tgatccta atcaattttca gcaaagaaca atattactta 60  
 tttcatcctg ttaaacttta gtatctatca gcataaagaa ttttataatg tcattcaatt 120  
 aaaatcctct ctataaaaaa atcaataatt cacctctaaa aaaaaacaaa agtgaatcat 180  
 gaatgaatga atgtgtacct tggcctagcc tgaactt 217

<210> 318  
 <211> 220  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_81016\_11  
  
 <400> 318  
  
 cctcggccaa acataactag tctaacagtt ttgtttgtat ctataattat tgtgtaaatg 60  
 attgtactta gagatccctc ttcattgaaa gagagagaga tgcccagact cctaaaaata 120  
 tctaaaatgc aataaaaatg attgtttgtt gtttgcatth aaaaaacagc aaacctttc 180  
 gtgctaaaat aaacttacca aacaagatgg aatcaaggct 220

<210> 319  
 <211> 222  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_134426\_14

<400> 319

ttacactatg ggtccgttcg gttataactt ttttaattctt atattaaata tattatcttt 60

aaaagactac tgatgaggat aaatacataa aaaaaaatag ttattttacc atctaaaaac 120

attgttccat tgagtacact tcaaatttag agaaaggaaa attgagttga aataatgaaa 180

tgaaatggat cataatccat catcatcttc cattatgttt ca 222

<210> 320

<211> 223

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292724\_14

<400> 320

ccattgtagg aggacaagaa tcacaagatc tctctctctc tctctctttc acatgaataa 60

atagaagaaa gagagaacaa caatctcaat atacacaaaa ctatgtatat ctatatgtac 120

atataatata taatatatga ttttggggga agtacttttt tctttgtgtg ttctgtgttg 180

ttgttgttgc tatggtatgc tattcacaaa gcaagagccg tta 223

<210> 321

<211> 225

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187096\_17

<400> 321

gtccagccaa atgcgtaaca tttattctga tgtaaaaaat tattattatt attatagata 60

ataaaatctt gttcctgaac aataaccatc aatgtaatta taaaattgaa tcttagactc 120

aaaactagtt attaactctgg aacaatgttt actcaaaact agttattaat agtattttta 180

agttaatttg aaattttttt ttcggcgtta aacaaatact agatg 225

<210> 322

<211> 228

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381693\_13

<400> 322

ttgatgttat gattcaatgg tttgatatgt ttcttagaaa gaaagaaaaa attgttgtaa 60

atatttagtac agtttgatac taaaactata atagtaaaat ttataataaa ctagaaaata 120  
 tactggatct tgtgttttct tactatttat gtcagacatt gtcagcctgc aaaatgaaga 180  
 tggatccttt tcaggggata tgtggggatga agttgatacg cggtatatt 228

<210> 323  
 <211> 229  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_361286\_33

<400> 323

actccagttg cattctcttc gtaaataaac cagtgtagtt agtataaata ttgtaagtac 60  
 ttaagccaaa catttgtgta ttttcattca ataggttctc tcattctctc tattgtgtgt 120  
 gtgtgtgtgt gtgtgtgtgt gtgtgttctg tgatatggat tcttatttct ggtatttttg 180  
 ctctttaacc tttaaaataa ttagggtaag caacaaagaa cacatttca 229

<210> 324  
 <211> 230  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_482668\_14

<400> 324

cgtttgttac ttcacacgca cacataaaaa aaaagtgtga ttatttcttt gttaaaattt 60  
 atctaaaagc attcaataaa ttaaattaaa caatcatttt tcttaataata gcagcaatct 120  
 tagtatagaa ttgaagttaa aaaaagtccc ttaataaggg aaaatacaat tgcacaacaa 180  
 ataattctct aaccaatcaa attttatggc acacttgtag gtaagtctga 230

<210> 325  
 <211> 231  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_128002\_12

<400> 325

cttgccaggg atcaaatcat aaagaaatat ttaccagtca aaaaagtcag aaatggagat 60  
 gcataacaat gttaaagtta gacaagtaaa taccocatat aaaatattta ctagaattct 120  
 agagagagag aggctgaatc tgttttctgt tattgattga tgaatcactt attactatct 180

gatggaagat gagttttata taatagagtt accttgtcct gcaagcttac a 231

<210> 326

<211> 239

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_499270\_14

<400> 326

cactgtgtaa gtgtcccttg catctccctg ctttattttg actgtaatgt gttgaattgt 60

ttatagtttc ttacttttca atgccaatat atatatatat gcttataatc ttctgtcaaa 120

atgctttctaa atctatgtat tttatgactt tgttaactat ataaaacatt tctaattatt 180

atcatgaatc tgacaattaa ttatacagat cagaaaacga gtctttctgat tcaaatccc 239

<210> 327

<211> 242

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_231650\_12

<400> 327

cttcaaggct ttggagaaca aacatgacaa gggaggagga ggaggaggag gagggagcgt 60

tgctgaatcc gacagcgact ccgaggagga ggagtacgag gacctggccc acaagcccat 120

tggccccgtg gacccctcca agtgcaccgc cgccgggacc gggatcgccg gcggaaccgc 180

gtgcgctccg tcctcctttg tgggtggtggc caaggacgcc gatgagagga aggtttccgg 240

tg 242

<210> 328

<211> 251

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_199851\_13

<400> 328

cggccatagt catatttatg cttccaaaag gccactactt ggatgaaaac ctccacttaa 60

tttaaagacc aattttctaa aaccatgcgt ttatttattt ataaaacccc tacgcggtaa 120

aaataaataa aaattgctag attttgattc tgccttctga aaaaggaagt gcacattagc 180

atattaatta aatattttct tccttctatt ttatttgata ttaaaactcac taatagcgtg 240

attggaaccc t 251

<210> 329  
 <211> 251  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_324629\_13

<400> 329

cggccatagt catatattatg cttccaaaag gccactactt ggatgaaaac ctccacttaa 60  
 tttaaagacc aatatttctaa aaccatgcgt ttatttattt ataaaacccc tacgcggtaa 120  
 aaataaataa aaattgctag attttgattc tgccttctga aaaaggaagt gcacattagc 180  
 atattaatta aatattttct tcttcttatt ttatttgata ttaaactcac taatagcgtg 240  
 attggaaccc t 251

<210> 330  
 <211> 266  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_374190\_19

<400> 330

agccaaggta aggcacacaa acttgccccc aggettttaa actctcttca cctgaaaata 60  
 aaaaataaaa taaaataaaa aataaaaaag ccaagttacc aaaaatacaa aatagtcaat 120  
 ccatataaac attcattatt tagatcttgt ttgtataaac ttctatataa aaacttttag 180  
 ggggaagtaa aaagtaaaat acattgagct tctcttataa gttaaaagca ggctagacag 240  
 atttctatta tcaccggatt ggatga 266

<210> 331  
 <211> 266  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_460603\_13

<400> 331

cacgcaacca ttcattgtac aaagttgttt ttataatcga aagaggaaac taagaaaaat 60  
 tactttcatg taagttataa gttagtttca taaactgtat taatgagggtt attataatta 120  
 ataaactgac aacagagtat aaattaaaat atctttattt atttatagaa attctctcaa 180

tacaaatggt tgtatcataa aataacataa caggtagatc attcctctga tgttattgag 240  
 attagcttgg gcagtattca atcctc 266

<210> 332  
 <211> 268  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_108681\_14

<400> 332

aagagtgtga aattggtacg acagttatta agtcatgtgg ataatgaaat taagagtaac 60  
 atttatgaaa atattatatt gagcaagtta taaacataat cactaaaact catcataaga 120  
 aaaaaaacat gattagtctt gacacataag ataaacatta atttaattta aaaaacaaag 180  
 aaaaaagtgt agagggggaga catatatattg acatttttta tttcaaaaga ataagagaaa 240  
 tatatatggt gcttgcacat tgatgaac 268

<210> 333  
 <211> 269  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_459791\_47

<400> 333

tgcttatgtc agctacgggc aatctttgat ttttttaata gagaaacatt ttttttacat 60  
 ctattattga gtgaacctta taataattta ttctttgaca tttattattg agtgaactaa 120  
 atgtaaatgt cataaagagt tactgaataa gaatatatat atatatatat atatatatat 180  
 atatatatat atatatatataa tatacatctt taacatttaa tgttcaacaa gttaactgaa 240  
 taataataga ggtacctact cgcctcgga 269

<210> 334  
 <211> 279  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_4257\_20

<400> 334

tccaacgca acagtaacgt aaatatttga agtgaaacta tactctttaa tcaaatgtac 60  
 tagtaactgt cacaaaattt aattcatata tatatatata tatatgcata ataataattt 120



ctctcatgca taagttttat tcttaattat tttttttcat aaattacttt atgttttcaact 180  
 atatatttta gaaaaaatg atattaaaaa agttaaatc taaaataaaa taagacttgc 240  
 taaataaaaa gattaggag tggttacatt caagtttca 279

<210> 335  
 <211> 288  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_238810\_14

<400> 335

caggtgttaa tactcctttc atttcaaaat attgatcggt ctagattttt tttaactgga 60  
 gttgttctag atatttttat ccaactaag aaaatataat aaatagataa aagaaaacag 120  
 taatttgata aaatcaattt tattattatt ttacaagcaa aaaaataagt aatgttatgt 180  
 taaaaatta aaacaataat tattttgaaa cttatttttg ttttacacga taattaatga 240  
 agagaattat atatatatat aaacgtcatc attggataga aacgatgt 288

<210> 336  
 <211> 289  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245817\_14

<400> 336

atcataaatt cattcaaaca catgctaaaa taaaagttta aatacttttt agtccttaat 60  
 ttagcttttt tgtttttggt tttgttttcg ttcttataaa cattttttgt tttgttttaa 120  
 tcttttttaa ttttttttat tttatttttc atcctcaaaa tgatttagat aacaaagaaa 180  
 aaaatattaa attacaagaa acaaaaaaat atataaacct aaaataaata taagagtaaa 240  
 agatatttat ttatttagct aaattgatct aaacacgcag aatggtagt 289

<210> 337  
 <211> 289  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245956\_14

<400> 337

atcataaatt cattcaaaca catgctaaaa taaaagttta aatacttttt agtccttaat 60

ttagctttttt tgtttttgtt tttgttttcg ttcttataaa cattttttgt tttgttttaa 120  
 tcttttttaa ttttttttat tttatttttc atcctcaaaa tgatttagat aacaaagaaa 180  
 aaaatattaa attacaagaa acaaaaaaat atataaacct aaaataaata taagagtaaa 240  
 agatatttat ttatttagct aaattgatct aaacacgcag aatggtagt 289

<210> 338  
 <211> 289  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74148\_14

<400> 338

tgcattgcatt taaccagaaa taataataac aattaacaac atgcattgcatt gcataaccggc 60  
 ttttttcata aaaaaaatg tttttacgtc cgtccaaatt attttatttt atatttcggc 120  
 ctttttagttt gtgattgatt ttgattaact ataaaataaa ttaatttcaa cacctattca 180  
 gtgtactttg tacacttatg ttaatttatt ttagagattt tctttttcta caatttctta 240  
 agtgagttaa aaaaatggtg attatttctt catacactct tgcagtgtg 289

<210> 339  
 <211> 289  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74089\_15

<400> 339

tgcattgcatt taaccagaaa taataataac aattaacaac atgcattgcatt gcataaccggc 60  
 ttttttcata aaaaaaatg tttttacgtc cgtccaaatt attttatttt atatttcggc 120  
 ctttttagttt gtgattgatt ttgattaact ataaaataaa ttaatttcaa cacctattca 180  
 gtgtactttg tacacttatg ttaatttatt ttagagattt tctttttcta caatttctta 240  
 agtgagttaa aaaaatggtg attatttctt catacactct tgcagtgtg 289

<210> 340  
 <211> 296  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_241686\_12

<400> 340

tggatcaaat ggtacttgtc aactgttttc ttttttaaaa aaatagcagg tatttgtcaa 60  
 cagtaagaag tatatagtct acatgtcaaa aagagtttac atataaagga ttaggtataa 120  
 caacttttaa gaataataaa agatgtaact tatagaaatg gtttttctat aactattaaa 180  
 aacaactttt taaatagtta taaaaaagt gacttaatta ttattatttt aaggagaact 240  
 ctttttttta ccaatttaag gaggacttaa ctgatgttaa taatgtgggc aaatgg 296

<210> 341  
 <211> 298  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_47476\_12

<400> 341

tttgcagcaa catatctgga ctttcttttt taccggtaga aaaatttcac atgtttttta 60  
 ttaaactaag atataacttt aatcttctta ttttgtaaat tcactatttt ttatctaatt 120  
 taaaattgag acgttttagtt ttcaggtttc gaaaatctct aatttttagtt cgatcttgaa 180  
 ttttgtcttc atttaatat attattataa gagaccaaaa cacaaataat atatgtattt 240  
 aaacctttat tttatgatca aaatatatgt ttgcaaacct gggcacataa tggaacac 298

<210> 342  
 <211> 299  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_164550\_12

<400> 342

caacataatc ctaatctccc atgcttaaat ttacccttat attcttataa gaaaaaaatc 60  
 acccgcatat ttttttccca ggtcatagat caatgtataa ctatggtttg tgtaaaaaag 120  
 ttttataact gatgaaaata tcaaatattt ctcccgtac atatttttat ttacctgaac 180  
 tcaacaaaac aaaaccttac gtatgagttt aaatgtacta atcgactaga gagagagagg 240  
 aaaaaaaag ataaaaatag aaataaatag acatttttat tcccggagga ccatatgtc 299

<210> 343  
 <211> 300  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_101255\_15

<400> 343

gcagtaatta agcctgtttc aacctgtaaa aaaaagtctg tttcaaaatt attttttatg 60  
 cattttactt aaaaaaatta gacctaatga attttgaata ttgatttgat ttttttaaga 120  
 gaatatattt ttgagttata tatatatata ttagtagtcc tacctcgttc taatatttta 180  
 tatttttttta ataaaatata caaatTTTTa aacaattttg tattaaggaa aaattaatca 240  
 ttttattcctt ataattatac aaaatttagc tttgaatgac cacatttaat tagtccatga 300

<210> 344

<211> 101

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_16189\_11

<400> 344

ttccacaaat ccaaattcca aattcatggt ctaacctcta acaactatat atatattcct 60  
 tgtcatttga tgagtatgct ttgatttcct atggaatctc a 101

<210> 345

<211> 108

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_71925\_13

<400> 345

tccgactttg tggctatata tgtgtgtggt tttgttcatt ttgtatttct ttctttctgc 60  
 aaaccatata gcagtataag tgttttgtaa tgtacatcgg gcacaact 108

<210> 346

<211> 110

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_4707\_12

<400> 346

caagatcaag cacccttggt tctctttttt ggattttatt gcaggttttg ttgttgttga 60  
 atcgtatttc tgttgcatca ttttttacac gctactgtct gtaatggaaa 110

<210> 347

<211> 111

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_118904\_18  
  
 <400> 347  
  
 tagctgcatc acctctcagt ttctgttagt ttagccaaat gcatgtatat aggacaaata 60  
  
 tatatatata tatattagct aaattgaaat cagggctaca tttaaggaca a 111  
  
  
 <210> 348  
 <211> 132  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_13655\_17  
  
 <400> 348  
  
 gagtcaattt ccttaaacc atcacatata atcaaattca aaatgtgtgt tgttaactca 60  
  
 ttggcaagtg gactaaattg tcacaagtaa taaaataaaa taaaagtctg agtatcaagt 120  
  
 ccacaggagc tt 132  
  
  
 <210> 349  
 <211> 143  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_53900\_13  
  
 <400> 349  
  
 atttcttcac atcgtcatcc caaacccaaa atctatagtt cttaactttc tacaatcaca 60  
  
 aacaaacaaa agcaatttaa aaccatagaa tagaacacaa cacccaataa agagcataaa 120  
  
 tcottacatt ccaccaagca cat 143  
  
  
 <210> 350  
 <211> 145  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_8079\_14  
  
 <400> 350  
  
 gtgagagtta agctgggaac ctttggcaac tcttgcaac tgtctcagaa agaataata 60  
  
 aataaataaa gccatcaaag agaccagaaa attctaccaa ttaggaaatc atgcaccaac 120  
  
 gcaagaggga agagagacag agatc 145

<210> 351  
 <211> 146  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_9969\_28

<400> 351

tcaccagaga cgcattatca gattcaaacc gaagaaaagg gagcaattag ggattattat 60  
 tattattatt attattatta ccagccgaag tcgttgccga gcgacatcgt ttgctaccg 120  
 tgagaaggaa acagtagctg gtagcg 146

<210> 352  
 <211> 147  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_72308\_77

<400> 352

tttcttaaac agatcactgg tatgcaaat ccatactata tatatatata tatatatata 60  
 tatatatata tatatatata tatatatata tatatatata tatatatata tatgataaga 120  
 acctctccc ttactactcc ctatgca 147

<210> 353  
 <211> 147  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_99475\_19

<400> 353

tgcacaatga gatttgaagt catgtaacga tcaacaaata acaagaataa tataatcaat 60  
 catgtaaaat aataataata ataatagaaa tcaagaacaa gtatgtccaa aaaatttagg 120  
 gagggtaatc gaagattcct gactcaa 147

<210> 354  
 <211> 147  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_118615\_18

<400> 354

atcatggatc tgattccacc tgaaaacaca attcagcaca actgagaatt ctgtattgcc 60  
 acaaacttaa ttttagttta gaacttattt ttacttagat ctttatatat atatatatat 120  
 acaacttagc gcccatatcat acaatca 147

<210> 355  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_119001\_46

<400> 355

tgaaatcagg gctacattta aggacaaata tatatatata tatatatata tatatatata 60  
 tatatatata gatagataga tagatagata gatagataga tagatagata gatagacatg 120  
 tacagcataa tcaagttgac caaatgcct 149

<210> 356  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_118958\_43

<400> 356

tgaaatcagg gctacattta aggacaaata tatatatata tatatatata tatatatata 60  
 tatatatata gatagataga tagatagata gatagataga tagatagata gatagacatg 120  
 tacagcataa tcaagttgac caaatgcct 149

<210> 357  
 <211> 149  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_17197\_13

<400> 357

cggagtcgga gtagtcgagt agacatagtg gggggcgata tcgcatagg atttattctc 60  
 tgggaggaat aattaattaa ttggtaatat attatTTTTT ttataatatt aatttattat 120  
 ataaagggtt catcggactc ggtattatg 149

<210> 358  
 <211> 150

<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_105163\_29

<400> 358

ttccaattcc ttagcctatc aaacatctaa tctaacatag agacgtaagg atctgccaat 60  
tctgatcata acaatcaacg caagtattcg atttcaataa taataataat aataataata 120  
ataagatggg aatgcatagg tacaaatgtt 150

<210> 359  
<211> 151  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_111335\_13

<400> 359

atacttaciaa tccgtcaggc agctcgatgc ttgcttgctt tgggggaata tttccaacgc 60  
ctgaggggctt tgagctcact gtggtctaata agacctcgtg aacctgctta gtctcacaac 120  
aaggttaciaa gagcgcaaac tcataacatg a 151

<210> 360  
<211> 152  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_106396\_13

<400> 360

ctgtcaaggg aggaaattgg tacagatcaa agtttggttg tactttgcc aactaaatatt 60  
atgacatcaa tagatactta gatagataga tgcctttatt tatctttggtt ttgaactact 120  
atgattactg gtactttctt ctggcagttg tt 152

<210> 361  
<211> 152  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_59229\_17

<400> 361

gcttgtcagg agagaaatgt tgcttaaaaa gaaaagaaaa gaatgaacga cgctaaaact 60  
agattgtatg tgaatgatag acagaagaat attaatatgt taaaattgac ctctttaaga 120



ttgaccact cccatgtttc atttgctgaa tt 152

<210> 362

<211> 153

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_73795\_20

<400> 362

tggcaacact taatttgac agataactct ctctctctct ctctctgaat taccacatgt 60

cttcaacata tttatagtag tactatatag ttaaaacaaa accacctaatt tattttttct 120

ttttagaaaa gggtttaatt tggtattctt ccc 153

<210> 363

<211> 153

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_85664\_20

<400> 363

tgtcaatcaa taaccattga tctccttacc tattcttaatt ttagttttta taatatagag 60

catttctaatt tgtatcgcta tatatatata tatatataaa taattgtatc gctataattt 120

attcttaatt tggtaccgt aaatagaaac caa 153

<210> 364

<211> 154

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_36921\_17

<400> 364

ccgagacca ctgtgtatta cttcagggtt cctcacgga acggaacaaa aggcgcacac 60

aatcgccaaa gagaaaaaga accctcaacc aaacaacaac aacaacaaaa aaaaagccct 120

agaaaagatt ttggagaagc aatttctcac tcct 154

<210> 365

<211> 155

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_124150\_19

<400> 365  
aagtggttgc acacagcatc taggaaaaaa gtcaaaaagc aacgctggat tagaacaaaa 60  
tataattatt gtttattttt ctttctttct ttctttttca ttttttaatg acatcttttt 120  
ccattgttgt aatggcagaa atcagtgttc agtga 155

<210> 366  
<211> 158  
<212> DNA  
<213> Glycine max  
<223> Seq ID: 515002\_region\_G2\_\_5089\_14

<400> 366  
tcatacctga aatatgggtg tcttcaaatt attagctaatt atttattttt tttaatcaag 60  
tagttgaaaa aaaaattcag tttcatttta ttattttattt atttttcatc aagtggtaat 120  
atgacatacg gagtggtgcc tcaacctgtc ttgttatg 158

<210> 367  
<211> 158  
<212> DNA  
<213> Glycine max  
<223> Seq ID: 515002\_region\_G2\_\_58221\_15

<400> 367  
catttcaaag ggagagccat catcatttta ttttattttt tgatatagag agccatcatt 60  
attgttgaaa ctaaagattt ctcataacat aaagttgtat actaagaaaa tgattgatat 120  
tcacttttag cattttcttt gctttctcca tttccatg 158

<210> 368  
<211> 161  
<212> DNA  
<213> Glycine max  
<223> Seq ID: 515002\_region\_G2\_\_96139\_14

<400> 368  
ccctcaagcc aatgatagta actccaaagt caaaaagttc agtatttttt ttttttttca 60  
ttttttcgtc agcttgaatg acacttggat ttagacaaag gttttttcat aataattata 120  
ataataataa ttttcacgta aggttgagca taggacgagt t 161

<210> 369  
 <211> 163  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_70595\_13

<400> 369

ttgggaactg tacacatgcc ttaatataat attatatttat tatattatat atgagtatatt 60  
 atatatttttt aatgtgatgg aaaaaagaag ataagaagaa aaatcagggtg agatgatata 120  
 agaatatata tatataataa ttccaaatga aataccacaa aca 163

<210> 370  
 <211> 166  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_4340\_15

<400> 370

aaatatgggt acatcatccg atacaattac taaactaaac taagggaaga attatttctca 60  
 cttttatatt tgttatttaa actatcaatt ctgaaatttc tattttgccc actaaccaaa 120  
 ttccctccacc ccctctcttt tcccttcctt ccttctcata tccaaa 166

<210> 371  
 <211> 169  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_90417\_11

<400> 371

aaactgcaaa cacaaattgc ctaaaataaa attgacaaac atgtaaactc ttttcatcac 60  
 cgaatagggt aatgggtagc caagagagag agataactga agggtaagaa tcagcagaaa 120  
 tcatcagaaa ggatatgaaa tgttaccaag tcaagtacag gctaccagg 169

<210> 372  
 <211> 169  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_49711\_17

<400> 372

caaagagagg cagaggaggt gattagatta gtgtcaactt gttgctatgc caacaatgac 60

aacccaaccc aacccatcta gagtacaaaa caaaggcaag acttttatgc cagcttttcc 120

tatatctaga gtagtactcc tacaatcaaa tgacaagcag ctacaacca 169

<210> 373

<211> 169

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_63053\_13

<400> 373

tgtgcataac tcgatctctt gatgatttct accaattggc ctcggcctta tatatatata 60

ttctcattct catatatata tatatgtgcg tgtagtttac atgaattttg caggtgatta 120

ttatttgaaa gcaaatttat ttatgctggt agtaaagatt gcagcaaga 169

<210> 374

<211> 169

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_63076\_14

<400> 374

tgtgcataac tcgatctctt gatgatttct accaattggc ctcggcctta tatatatata 60

ttctcattct catatatata tatatgtgcg tgtagtttac atgaattttg caggtgatta 120

ttatttgaaa gcaaatttat ttatgctggt agtaaagatt gcagcaaga 169

<210> 375

<211> 171

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44442\_12

<400> 375

aacgcgtctt tctttcttct tcaactaatt tgcattaaaa gtatcctcaa gtaactaaga 60

aagcaatcaa gaaagaaagc ttcttgtatt cattcattca ttattatgt gtgtgtgtgc 120

gagtacaaaa tttatttctg gaatctgagg tgtttcatat agccatgttg c 171

<210> 376

<211> 171

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44422\_19

<400> 376

aacgcgtctt tctttcttct tcaactaatt tgcattaaaa gtatcctcaa gtaactaaga 60  
aagcaatcaa gaaagaaagc ttcttgtatt cattcattca ttcattatgt gtgtgtgtgc 120  
gagtacaaaa tttatttctg gaatctgagg tggttcatat agccatgttg c 171

<210> 377

<211> 178

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44158\_19

<400> 377

tttcattacg tgcgtttgta caactactat gaaacaaaca tgaaaaatgc acaatttact 60  
cgtagaaata ataataataa taaaaataaa taaataaata aaataaagta ttttttgaaa 120  
aataaaagat tgtagtact agttactacg gagtatcgta ttcgtatcat ccaccctg 178

<210> 378

<211> 178

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44141\_17

<400> 378

tttcattacg tgcgtttgta caactactat gaaacaaaca tgaaaaatgc acaatttact 60  
cgtagaaata ataataataa taaaaataaa taaataaata aaataaagta ttttttgaaa 120  
aataaaagat tgtagtact agttactacg gagtatcgta ttcgtatcat ccaccctg 178

<210> 379

<211> 178

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_90762\_17

<400> 379

ccagagatat gattcaatac aaaggaaatt aagtaaacac taactcaaca ttctaaattt 60  
tctttacttt tctctattaa tattttttta aaaagaaaat tcttctcaca tatacaaaga 120  
gtcttgaggg agggaggag ggcaatgcc ccccttgaat ccgttaccac agggtaat 178

<210> 380  
 <211> 182  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_106241\_14

<400> 380

tagatagcta gccatgttgg catgaagatt tgagcgggaa aataataaga caacatacat 60  
 aacgttttct caaagtgggt tttttatttt atttttttta tcataagggt ttgcttttta 120  
 gttttttatt tttcagtttt tgtggataat tctattaact gtcaagggag gaaattggta 180  
 ca 182

<210> 381  
 <211> 185  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_109676\_12

<400> 381

tcattgtctt tgaggacttt ctcatatta ttggatttta atcaataact tcttctactg 60  
 tcttcttgag agagagagat gggggaaatt tgaaactgca ttcatatttt acagttttta 120  
 tacattatgc aagattttact caaatgcttt ttgtacttaa aatggctatc actcagtgtc 180  
 agtga 185

<210> 382  
 <211> 185  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_86242\_14

<400> 382

ccacaactcc gatttatccc ataacaataa gtaaataata agtaaaatgg acatgagttt 60  
 tagcaaaaaa aaatagaaaa actaagcata ctaaaacatt atcattttta gaaagaaaga 120  
 aaaaagacta tcataactga ttaggatcat aaaatttcct gaaactccaa atttcttctt 180  
 tgtgc 185

<210> 383  
 <211> 186

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 515002\_region\_G2\_\_83109\_12  
 <400> 383  
 tcacccttta ggagatccta gacacttatg gaaaagtatc aagacaactt atcaattttc 60  
 aaaagtctga aatctttttg agttcgatta ttcaacaaca acaaagacac aaaatctctt 120  
 cctaggtgtc actaaaagca ttggatccaa caaatattta ggacttcctt caatcattgg 180  
 caagag 186

<210> 384  
 <211> 192  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 515002\_region\_G2\_\_10461\_15  
 <400> 384  
 ggctgtgtgt gagtgagagt gagagtgaga gtgagggtgg ataaaacaaa caaacaaaac 60  
 tagcgcatth tggtgcgggt ggaattagac tgttactaag tgcttaatta atgggggaaag 120  
 gaaagtggta tgattagtgt ttgtaacagt aagtgattat tgtaaatgat gattaggagg 180  
 aataagggtg ca 192

<210> 385  
 <211> 194  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 515002\_region\_G2\_\_67608\_15  
 <400> 385  
 ggtgggttaga tccaatttca tggtgaattt aatattgtgg aacaaaaagg cggtgttata 60  
 tatatatata tgatggtcga tggcgcaaga ggggatcgga agattatact taaagaagca 120  
 gaagcatact tgtactccaa tctaataaaa atgttctata tataatagaa aatacggata 180  
 cgtgctgtac agga 194

<210> 386  
 <211> 200  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 515002\_region\_G2\_\_63275\_46

<400> 386  
 tgctgttagt aaagattgca gcaagatttt gccataatta aaaatctact ttaaccccat 60  
 tgccctgcat gtacatttta ttattagttt gtttgatgat tttggaattt tgtggtttaa 120  
 tttattaata tatatatata tatatatata tatatatata tatatgtata tattttgaag 180  
 gaattgagga gcggagtata 200

<210> 387  
 <211> 203  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_62405\_14

<400> 387  
 tgcatagaga gaaatagacg aggaaaaata taaaagaaaa gaaaaaaatt ataaataaaa 60  
 caaacaacat aataaaaaat gaaaagaaga atagaaggaa aaatagactc aaaatgagat 120  
 tttgaaatta tataattaat aatccaatta atctcatgag atattattct ataactataa 180  
 cttatggacc gtttgaaga gat 203

<210> 388  
 <211> 211  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_33563\_12

<400> 388  
 ccttaggtgc tcatacatcc aaacacttac acacttgttt tagtaaataa tggttatatc 60  
 tatctcaa ataatccaatg tttagaataa atccttgatt gacttattat tattaatatg 120  
 ctcatattata aattattgtc aaagataatt ttgttgaaca aattttttta atatttacia 180  
 aatatacggtt tcttgcggtg tatatgaatc a 211

<210> 389  
 <211> 243  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_33146\_14

<400> 389  
 cgaaccctaa acatttcaaa ccaaattact cacagatata gtttttttca aaaattgatt 60



gagagatcgt gtagaaaaag taaatttcaa gcaaaaactca tcctcaatat ccttttttgta 120  
 ttggtttata aacatgagag aattgggaaa acgcttttgt tttttgatcc attctcacat 180  
 ctgcgatttt gcttcttttt ctttctttct tccatgtatg tgtttccaac ctttcttctg 240  
 aaa 243

<210> 390  
 <211> 251  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_102179\_29

<400> 390

aatctcgatt gtcttcttgc gaaattgatt tccatcgatt tctctctatt ttttcttttc 60  
 taaattatat tgacaactat atatatatat atatatatat atatattatg taacaaatth 120  
 tatgatgcag ttagataaca agaatcaaac aataaaaata tataaaaata agcttaagta 180  
 attaatatcc ctaaaattaa atcagataaa ttaaaatggt ttgtatattg cttgattgth 240  
 gacttggttg a 251

<210> 391  
 <211> 257  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_2646\_15

<400> 391

ccaaaggctt agtttcatth gcattaacat attaataata attcacaaga gaagaaatth 60  
 aaaataagat aaatcaatth tttcacaagt taaatthtat tttatthttt ggaatthtta 120  
 caagaaataa aaaaattcat aacttaaaat taactcatgt atgataactt tttatagth 180  
 tttttgttta atthttcctaa aagataaggc gtataaatta atthtagtht acgagagaag 240  
 ttggatthgt ttattht 257

<210> 392  
 <211> 269  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_76652\_24

<400> 392

actaactctt gcgtgctcct tgtttcaaac aattaaatta atataagggt atttgttagt 60  
 gtttaggata ttggttaaga aatcaatata tatatatata tatatatatt gtataaatta 120  
 taagagaata taaaaaaatt atgaatagta taattttttg tttttcaatt tttaaaattt 180  
 taattaaagg aaaattgggt atatttaaaa ttattcttta tgtagaagaa aaattgataa 240  
 atgattttga tccagtatat gtcccaggg 269

<210> 393  
 <211> 283  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_66280\_14

<400> 393

gtgttagatt gattaaagtt cgctgatata acttttattt aatgaaaatt aaattgttag 60  
 tacaaatatt gcaagtcttt attaataata caatacatca tactaacata tccaaaatat 120  
 ttatactaatt taacagttca atcctgctag ataaatgctt ttctatatat acactgacag 180  
 aacagtttta atgctttttt aattttttcc tgtttgtaatt aatgattttt tgtttgtttg 240  
 ttagaaattg acattttttt cactttaatc atgggctaaa tct 283

<210> 394  
 <211> 284  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_54768\_13

<400> 394

aaattaccaa tcatgtatgg agtgagaaaa cctcgagcat atgagaaagg ggtatatgaa 60  
 tatactacta ttcgtattat tatcaaatat taatatgttc catagaaatt tacaaattat 120  
 ttatatctta ttattattat ttagtaatag tagtatagta ttagtaatga cattggatcg 180  
 taaatgtaaa ttaaatatta tatcattagt atttgtagga atgtaaaatt taattttaat 240  
 gaaaaatatt atatgacaaa agttatgggtg caatattgtg cctg 284

<210> 395  
 <211> 289  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_62580\_14

&lt;400&gt; 395

aacttatgga ccgtttggaa gagataaaaa aagaaaagaa aatattgatt acaatatatt 60  
 tttctttggt taattgaaga aaaataaaga aacaattgac ttctaagaat aaaaattcaa 120  
 aacttttctt atgttttaac ttttttttaa tttcaaattt tccttttctt gatttttctt 180  
 tcccactaca attgactgag tcagactgaa cgtgatactt agatacatat atgcaactct 240  
 cagtactact cctcacctct atataatctt cactctttgc tcctccttt 289

&lt;210&gt; 396

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 515002\_region\_G2\_\_34598\_55

&lt;400&gt; 396

aaagtctggt ctgaactgac ccatttaatt aagagggttag gttcaagctt ttttaaaaag 60  
 cttattaaat taaatagatc agacttaggc ttgttaaaaa gccttataag tctgataggt 120  
 cggcctatat atatatatat atatatgtat atgtatatat atatatatat gtatatatat 180  
 ttatattatt tgttgatacc aatttatact tatattattt tttgggtaca attaatTTTT 240  
 ttttgaaacc agcagacttt gattatacat tactgctcca taacttccat tcc 293

&lt;210&gt; 397

&lt;211&gt; 298

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 515002\_region\_G2\_\_77680\_13

&lt;400&gt; 397

tgacatgaac tatctcaaac aatgcaaaaa ttgtcccctt aaaggcaata ccccctttcc 60  
 cccccttaaa atttggcttt caaaaagtac ttttttcaaa atacattaat ttttaacatg 120  
 gctagaaagt atttttgaaa tattaataatt ttaacacttc cagaaaaatat tttctgaaat 180  
 gtgttgaaat tttttaatct gttttgaaaa gtagtttcca aaaaagagat acttgtagaa 240  
 gaagaagaat atatatatat agtattagta aatctgggag gtgtaaataa cagttggt 298

&lt;210&gt; 398

&lt;211&gt; 298

&lt;212&gt; DNA

&lt;213&gt; Glycine max

<223> Seq ID: 515002\_region\_G2\_\_\_77693\_12

<400> 398

```

tgacatgaac tatctcaaac aatgcaaaaa ttgtcccctt aaaggcaata cccctttcc 60
cccccttaaa atttggtttt caaaaagtac ttttttcaaa atacattaat ttttaacatg 120
gctagaaaagt atttttgaaa tattaaaatt ttaacacttc cagaaaatat tttctgaaat 180
gtgttgaaat tttttaatct gttttgaaaa gtagtttcca aaaaagagat actttagtaa 240
gaagaagaat atatatatat agtatttagta aatctgggag gtgtaaataa cagttgtt 298

```

<210> 399

<211> 300

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_\_97392\_14

<400> 399

```

tttgatgtag ttgatttatg cactcgattg tacaaatata attgttttta aatattgtgc 60
aaatgggttt tggggatttc acttacttaa tatgatttag aaacattatt attattattt 120
ctgtaaaaaa aaagaaatat tattattatt acaatttctt catccttctt atatactttt 180
ttaaaaacga aaaaaaaaaa tattgagttt cgtttatgat taagaaaaat gtttcataat 240
taaaaattaa aaactagtgt ctgcatcatc acattactaa actagggtgc ctgatgtcac 300

```

<210> 400

<211> 300

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_\_97359\_15

<400> 400

```

tttgatgtag ttgatttatg cactcgattg tacaaatata attgttttta aatattgtgc 60
aaatgggttt tggggatttc acttacttaa tatgatttag aaacattatt attattattt 120
ctgtaaaaaa aaagaaatat tattattatt acaatttctt catccttctt atatactttt 180
ttaaaaacga aaaaaaaaaa tattgagttt cgtttatgat taagaaaaat gtttcataat 240
taaaaattaa aaactagtgt ctgcatcatc acattactaa actagggtgc ctgatgtcac 300

```

<210> 401

<211> 25

<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_289711\_11\_Forward\_Primer  
  
<400> 401  
  
aaaccttgac gttgttgtct ttggt 25  
  
<210> 402  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_289711\_11\_Reverse\_Primer  
  
<400> 402  
  
ggaatattgt accaatcacc cggta 25  
  
<210> 403  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_236585\_14\_Forward\_Primer  
  
<400> 403  
  
agtcgggag attagttgca gtaaa 25  
  
<210> 404  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_236585\_14\_Reverse\_Primer  
  
<400> 404  
  
tgaagatctg aatctgattg cctga 25  
  
<210> 405  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_168772\_13\_Forward\_Primer  
  
<400> 405  
  
tttgcattgt ttcaatttat ttcca 25

<210> 406  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_168772\_13\_Reverse\_Primer  
  
<400> 406  
  
aatttcaacc aacagacatt gagtga 26  
  
<210> 407  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_332420\_21\_Forward\_Primer  
  
<400> 407  
  
gagaatctgc aactgaacca aatga 25  
  
<210> 408  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_332420\_21\_Reverse\_Primer  
  
<400> 408  
  
acttaggaat ggaacagcag actgg 25  
  
<210> 409  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_228126\_18\_Forward\_Primer  
  
<400> 409  
  
atagctctgt tgcaaaggaa gatgg 25  
  
<210> 410  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_228126\_18\_Reverse\_Primer  
  
<400> 410  
  
attggcatgc aagatatcag gagaa 25

<210> 411  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_139723\_11\_Forward\_Primer  
  
 <400> 411  
  
 ttgcattcaa attcatggaa ctacc 25  
  
 <210> 412  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_139723\_11\_Reverse\_Primer  
  
 <400> 412  
  
 tcaccatgtg tgcataaataac 25  
  
 <210> 413  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_280585\_14\_Forward\_Primer  
  
 <400> 413  
  
 tttacaagtg catcatttaa cttctca 27  
  
 <210> 414  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_280585\_14\_Reverse\_Primer  
  
 <400> 414  
  
 tttggcctca atttaaagat cctgt 25  
  
 <210> 415  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_70509\_14\_Forward\_Primer  
  
 <400> 415

cctatgaaga atacacccac gttga 25

<210> 416

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_70509\_14\_Reverse\_Primer

<400> 416

cagcctccat caggaagatg aatac 25

<210> 417

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_50537\_17\_Forward\_Primer

<400> 417

aaacccaaca taattccaac ttcaa 25

<210> 418

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_50537\_17\_Reverse\_Primer

<400> 418

agcagagcat cccaaattaa tgcta 25

<210> 419

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_231556\_17\_Forward\_Primer

<400> 419

agcccttcca caaactagag cgtat 25

<210> 420

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_231556\_17\_Reverse\_Primer



<400> 420  
ttctgccgaa acacttccag taaat 25

<210> 421  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_117057\_11\_Forward\_Primer

<400> 421  
aaagacggaa cagcgtcaaa taaac 25

<210> 422  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_117057\_11\_Reverse\_Primer

<400> 422  
gacggaaaca cgctctacaa ttaca 25

<210> 423  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_23092\_13\_Forward\_Primer

<400> 423  
tcaataggta ctggcacaag acacc 25

<210> 424  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_23092\_13\_Reverse\_Primer

<400> 424  
ttagcccttt atgtcctctc attcc 25

<210> 425  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_297741\_14\_Forward\_Primer  
<400> 425  
tttataaatc tgtccagcca ccaaa 25  
  
<210> 426  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_297741\_14\_Reverse\_Primer  
<400> 426  
agaactagat tggatatgcc gtgct 25  
  
<210> 427  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_206502\_14\_Forward\_Primer  
<400> 427  
agaagaagac gacgacatcg aagag 25  
  
<210> 428  
<211> 20  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_206502\_14\_Reverse\_Primer  
<400> 428  
ggacaggggt tccagcttcg 20  
  
<210> 429  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_221223\_13\_Forward\_Primer  
<400> 429  
ccagagtctt gtaagaaagc catca 25  
  
<210> 430  
<211> 25

<212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_221223\_13\_Reverse\_Primer  
 <400> 430  
 cagctgacac atgtccattc tttct 25

<210> 431  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_169084\_14\_Forward\_Primer  
 <400> 431  
 tttgcttgaa taaatgtgca cagaa 25

<210> 432  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_169084\_14\_Reverse\_Primer  
 <400> 432  
 gcaaagggttg ctccttctga attt 24

<210> 433  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_94891\_14\_Forward\_Primer  
 <400> 433  
 catcaacaaa tcacacacac acaca 25

<210> 434  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_94891\_14\_Reverse\_Primer  
 <400> 434  
 tccaactgaa gagaagaagg cattg 25

<210> 435  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_7439\_12\_Forward\_Primer  
  
<400> 435  
  
ggtgctgtag tgcttgaaac agttg 25  
  
<210> 436  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_7439\_12\_Reverse\_Primer  
  
<400> 436  
  
accaatgtaa atgcgaacac agaaa 25  
  
<210> 437  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_281852\_61\_Forward\_Primer  
  
<400> 437  
  
aaccagagga aacagggagt cattt 25  
  
<210> 438  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_281852\_61\_Reverse\_Primer  
  
<400> 438  
  
cagtctttca ttaatcctcc gtcgt 25  
  
<210> 439  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_46583\_12\_Forward\_Primer  
  
<400> 439  
  
gtaacaaatt ctgaaccctg catgt 25

<210> 440  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_46583\_12\_Reverse\_Primer  
  
<400> 440  
  
tgtgttgcaa gttgaagaat ggttt 25  
  
<210> 441  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_306835\_13\_Forward\_Primer  
  
<400> 441  
  
agtctcccag atgatcaatt ctgct 25  
  
<210> 442  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_306835\_13\_Reverse\_Primer  
  
<400> 442  
  
aatcacatc caagacgtga aactaa 26  
  
<210> 443  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_85471\_12\_Forward\_Primer  
  
<400> 443  
  
cgtggccact tgatctataa gagag 25  
  
<210> 444  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_85471\_12\_Reverse\_Primer  
  
<400> 444

atattagctt ctttgctttc ccttg 25

<210> 445  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_257208\_12\_Forward\_Primer

<400> 445

ccatgaatga aactcaccaa actga 25

<210> 446  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_257208\_12\_Reverse\_Primer

<400> 446

aattactatg attctggctg gcaca 25

<210> 447  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150390\_17\_Forward\_Primer

<400> 447

ttacgcactc agatttgat ttgat 25

<210> 448  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150390\_17\_Reverse\_Primer

<400> 448

agggtgtgaa gtttaatcac catga 25

<210> 449  
<211> 24  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_34697\_75\_Forward\_Primer

<400> 449  
 gcatgctctt aggtgattgc agag 24

<210> 450  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_34697\_75\_Reverse\_Primer

<400> 450  
 ttcatagaagg cagttgaatg tatcc 25

<210> 451  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150374\_13\_Forward\_Primer

<400> 451  
 ttacgcactc agatttggat ttgat 25

<210> 452  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_150374\_13\_Reverse\_Primer

<400> 452  
 aggtgtgaa gtttaatcac catga 25

<210> 453  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_40513\_22\_Forward\_Primer

<400> 453  
 attctgaaat tgggtgaagg ttctg 25

<210> 454  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_40513\_22\_Reverse\_Primer  
<400> 454  
caaataaatg tgaagccaca cctga 25

<210> 455  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_268602\_14\_Forward\_Primer  
<400> 455  
aacacgtctc atctcaagaa gctca 25

<210> 456  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_268602\_14\_Reverse\_Primer  
<400> 456  
taacttcgac caaataggcc tagca 25

<210> 457  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_25357\_13\_Forward\_Primer  
<400> 457  
acttctccca cactttccct ttctc 25

<210> 458  
<211> 21  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_25357\_13\_Reverse\_Primer  
<400> 458  
agcggaaatct cctctggctt c 21

<210> 459  
<211> 24



<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_137548\_13\_Forward\_Primer  
  
<400> 459  
  
gtatgaaccc taaagctggc ttcg 24  
  
<210> 460  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_137548\_13\_Reverse\_Primer  
  
<400> 460  
  
gcacagattt gttaagagga atgct 25  
  
<210> 461  
<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_139131\_13\_Forward\_Primer  
  
<400> 461  
  
gtatgaaccc taaagctggc ttcg 24  
  
<210> 462  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_139131\_13\_Reverse\_Primer  
  
<400> 462  
  
gcacagattt gttaagagga atgct 25  
  
<210> 463  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_203855\_12\_Forward\_Primer  
  
<400> 463  
  
ttgttgtcaa gagaaggga gctct 25

<210> 464  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_203855\_12\_Reverse\_Primer  
  
 <400> 464  
  
 tcatgtgctc acatctgtgt tgttt 25  
  
 <210> 465  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_199049\_15\_Forward\_Primer  
  
 <400> 465  
  
 ggcaaatac atgtacataa gggaga 26  
  
 <210> 466  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_199049\_15\_Reverse\_Primer  
  
 <400> 466  
  
 tcaccaaata aactcactga gcaaa 25  
  
 <210> 467  
 <211> 22  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_320907\_12\_Forward\_Primer  
  
 <400> 467  
  
 gattcgccgg aaattctctc ct 22  
  
 <210> 468  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_320907\_12\_Reverse\_Primer  
  
 <400> 468  
  
 ctccgatatt aagctcgcca tcct 24

<210> 469  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_16407\_17\_Forward\_Primer  
  
 <400> 469  
  
 cacactctca cagcaacttc tcgat 25  
  
 <210> 470  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_16407\_17\_Reverse\_Primer  
  
 <400> 470  
  
 atatcactga tccacgtggg atttc 25  
  
 <210> 471  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_206516\_17\_Forward\_Primer  
  
 <400> 471  
  
 cagaagacga agacgaagaa gagga 25  
  
 <210> 472  
 <211> 20  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_206516\_17\_Reverse\_Primer  
  
 <400> 472  
  
 actcggattg ggaccagctc 20  
  
 <210> 473  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_264495\_13\_Forward\_Primer  
  
 <400> 473

agtggcataa agcaagaagt tcacc 25

<210> 474  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_264495\_13\_Reverse\_Primer

<400> 474

gagattcaag ggaatgcata ctgaa 25

<210> 475  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_156785\_13\_Forward\_Primer

<400> 475

atctagtgcc tccacgcatac tctac 25

<210> 476  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_156785\_13\_Reverse\_Primer

<400> 476

gttggcgcttg aagagagaga aagag 25

<210> 477  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_187129\_12\_Forward\_Primer

<400> 477

tgattgggaa ggaaagcttc attag 25

<210> 478  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_187129\_12\_Reverse\_Primer

<400> 478  
atttatcttg caccatgacc aaacc 25

<210> 479  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_214106\_13\_Forward\_Primer

<400> 479  
ccatcttctt ctcaatcctc atgttg 26

<210> 480  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_214106\_13\_Reverse\_Primer

<400> 480  
gttttaaagta gagcacgagg agagc 25

<210> 481  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_149013\_12\_Forward\_Primer

<400> 481  
aagctcaacg tggatgtttg ttaga 25

<210> 482  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_149013\_12\_Reverse\_Primer

<400> 482  
gcacactaga catttatttc gctttga 27

<210> 483  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_326352\_16\_Forward\_Primer  
<400> 483  
gttggttacct tgtgtgttcg ctttg 25

<210> 484  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_326352\_16\_Reverse\_Primer  
<400> 484  
agggttgtgg aagcaagttc atatc 25

<210> 485  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_278962\_12\_Forward\_Primer  
<400> 485  
tcgaatctat cgcggaatac tcaat 25

<210> 486  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_278962\_12\_Reverse\_Primer  
<400> 486  
tttccttagc tcaatttgca actcc 25

<210> 487  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_256930\_13\_Forward\_Primer  
<400> 487  
tgtgacctat ctttcctccg ttctc 25

<210> 488  
<211> 25

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_256930\_13\_Reverse\_Primer  
  
 <400> 488  
  
 tcccaagtct gataaggtaa accaa 25  
  
  
 <210> 489  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_29646\_14\_Forward\_Primer  
  
 <400> 489  
  
 acgcaactca gatgcattaa cacaa 25  
  
  
 <210> 490  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_29646\_14\_Reverse\_Primer  
  
 <400> 490  
  
 tgaataatga tcatcgtcca ctgata 26  
  
  
 <210> 491  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_29618\_13\_Forward\_Primer  
  
 <400> 491  
  
 acgcaactca gatgcattaa cacaa 25  
  
  
 <210> 492  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_29618\_13\_Reverse\_Primer  
  
 <400> 492  
  
 tgaataatga tcatcgtcca ctgata 26

<210> 493  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_108561\_14\_Forward\_Primer  
  
<400> 493  
  
aatgttgctt gccttcacag ctaag 25  
  
<210> 494  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_108561\_14\_Reverse\_Primer  
  
<400> 494  
  
tccaaaccct tattcataac ccaga 25  
  
<210> 495  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_143975\_14\_Forward\_Primer  
  
<400> 495  
  
cggtagctat agcgtattgc aacaaa 26  
  
<210> 496  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_143975\_14\_Reverse\_Primer  
  
<400> 496  
  
cccatcgta gtagtatcac attca 25  
  
<210> 497  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_108431\_20\_Forward\_Primer  
  
<400> 497  
  
ccgaatgaca gagaggaaga agaaa 25



|                             |  |    |
|-----------------------------|--|----|
| <210>                       | 498  |    |
| <211>                       | 24   |    |
| <212>                       | DNA  |    |
| <213>                       | Glycine max  |    |
| <223>                       | Seq ID: 240017_region_G3__108431_20_Reverse_Primer |    |
| <400>                       | 498  |    |
| atttcaactt cccacaccac tgac  |  | 24 |
|                             |  |    |
| <210>                       | 499  |    |
| <211>                       | 25   |    |
| <212>                       | DNA  |    |
| <213>                       | Glycine max  |    |
| <223>                       | Seq ID: 240017_region_G3__281764_11_Forward_Primer |    |
| <400>                       | 499  |    |
| ttcctggtga gtaacaagtg taggg |  | 25 |
|                             |  |    |
| <210>                       | 500  |    |
| <211>                       | 25   |    |
| <212>                       | DNA  |    |
| <213>                       | Glycine max  |    |
| <223>                       | Seq ID: 240017_region_G3__281764_11_Reverse_Primer |    |
| <400>                       | 500  |    |
| tctggttcat gctctattca aacga |  | 25 |
|                             |  |    |
| <210>                       | 501  |    |
| <211>                       | 25   |    |
| <212>                       | DNA  |    |
| <213>                       | Glycine max  |    |
| <223>                       | Seq ID: 240017_region_G3__130058_15_Forward_Primer |    |
| <400>                       | 501  |    |
| agtctcgctc ctatttcgag tcctt |  | 25 |
|                             |  |    |
| <210>                       | 502  |    |
| <211>                       | 25   |    |
| <212>                       | DNA  |    |
| <213>                       | Glycine max  |    |
| <223>                       | Seq ID: 240017_region_G3__130058_15_Reverse_Primer |    |
| <400>                       | 502  |    |

gtgccacctt gaatccactt atcat 25

<210> 503

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_310590\_52\_Forward\_Primer

<400> 503

ttccctaata atggtggaag cagtt 25

<210> 504

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_310590\_52\_Reverse\_Primer

<400> 504

acccaaaccc aatatggtgt tctac 25

<210> 505

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_313405\_14\_Forward\_Primer

<400> 505

cggatgttaa atgattggtt cgttt 25

<210> 506

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_313405\_14\_Reverse\_Primer

<400> 506

aattatgttg gactggttct ggaaa 25

<210> 507

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_302190\_13\_Forward\_Primer

<400> 507  
ttaaaccact accaaatata ctccaaa 27

<210> 508  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_302190\_13\_Reverse\_Primer

<400> 508  
caagttcggg taggatgaac acgat 25

<210> 509  
<211> 24  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_225343\_17\_Forward\_Primer

<400> 509  
cccgcaattt gttatagtgg gaaa 24

<210> 510  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_225343\_17\_Reverse\_Primer

<400> 510  
agtaaagtgc acttcaaacg catgg 25

<210> 511  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_208823\_14\_Forward\_Primer

<400> 511  
tactttccaa attgatgcag accag 25

<210> 512  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_208823\_14\_Reverse\_Primer  
<400> 512  
tgtcccaa at agggagttac aagga 25  
  
<210> 513  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_74285\_11\_Forward\_Primer  
<400> 513  
tgatgaca at gatgacgatt tgtga 25  
  
<210> 514  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_74285\_11\_Reverse\_Primer  
<400> 514  
aattcatctg caacgtcctg gtaag 25  
  
<210> 515  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_109052\_16\_Forward\_Primer  
<400> 515  
cacatttgat gattgattcc agttt 25  
  
<210> 516  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_109052\_16\_Reverse\_Primer  
<400> 516  
ccataatgtc agtgctttct ggcta 25  
  
<210> 517  
<211> 25

<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_6395\_12\_Forward\_Primer

<400> 517

tactactgaa ccgtggtgcc tgata 25

<210> 518  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_6395\_12\_Reverse\_Primer

<400> 518

gccatacaaa tgcattgtgg ttaat 25

<210> 519  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_244905\_16\_Forward\_Primer

<400> 519

tgaaatccaa gtgaaagatt gttaaa 26

<210> 520  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_244905\_16\_Reverse\_Primer

<400> 520

tatgcgtatt acctccaacg tccat 25

<210> 521  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_244956\_13\_Forward\_Primer

<400> 521

tgaaatccaa gtgaaagatt gttaaa 26

<210> 522  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_244956\_13\_Reverse\_Primer  
  
<400> 522  
  
tatgcgtatt acctccaacg tccat 25  
  
<210> 523  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_117220\_13\_Forward\_Primer  
  
<400> 523  
  
aagagaattg gcaaagtgca gtagc 25  
  
<210> 524  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_117220\_13\_Reverse\_Primer  
  
<400> 524  
  
ctcccatctt cttcactctc agcat 25  
  
<210> 525  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_134707\_14\_Forward\_Primer  
  
<400> 525  
  
tgtacatcaa actggcaagg aagag 25  
  
<210> 526  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_134707\_14\_Reverse\_Primer  
  
<400> 526  
  
gagattgcac agaagggaaa ttggtt 25

<210> 527  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_35078\_13\_Forward\_Primer  
  
 <400> 527  
  
 agcaagatca gaagtcgcaa acac 24  
  
 <210> 528  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_35078\_13\_Reverse\_Primer  
  
 <400> 528  
  
 ctcccattct tccatttcca tttct 25  
  
 <210> 529  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_210506\_16\_Forward\_Primer  
  
 <400> 529  
  
 ttgatattgt tgcaaatacac ctgaa 25  
  
 <210> 530  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_210506\_16\_Reverse\_Primer  
  
 <400> 530  
  
 gaggtcaagt aagtgcacac tcaga 25  
  
 <210> 531  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_116961\_26\_Forward\_Primer  
  
 <400> 531

atccgggaaa tgattctaaa catga 25

<210> 532

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_116961\_26\_Reverse\_Primer

<400> 532

gtttatttga cgctgttccg tcttt 25

<210> 533

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_51073\_13\_Forward\_Primer

<400> 533

caaattgccca catttctcat gtcag 25

<210> 534

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_51073\_13\_Reverse\_Primer

<400> 534

gtgtgtagag gctaaggctt gagga 25

<210> 535

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_55291\_15\_Forward\_Primer

<400> 535

ccctagggac aacagggtac ctaat 25

<210> 536

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_55291\_15\_Reverse\_Primer



<400> 536  
atggtcctga ctcgtgtaac caaat 25

<210> 537  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_229651\_18\_Forward\_Primer

<400> 537  
acaatcaagg aatctaagcc acaca 25

<210> 538  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_229651\_18\_Reverse\_Primer

<400> 538  
ctgttcttgc agtaatgttg gcact 25

<210> 539  
<211> 24  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_303308\_19\_Forward\_Primer

<400> 539  
caactcctct ttcaattcgc acac 24

<210> 540  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_303308\_19\_Reverse\_Primer

<400> 540  
tgtggaattt gttgtgtcta agggta 26

<210> 541  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_168373\_20\_Forward\_Primer

<400> 541

gaacaggcta tcatggctga agaag 25

<210> 542

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_168373\_20\_Reverse\_Primer

<400> 542

atcagatgat gctgaatgct tgtgt 25

<210> 543

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_253333\_17\_Forward\_Primer

<400> 543

gtcatcaccc atataaactt gtcca 25

<210> 544

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_253333\_17\_Reverse\_Primer

<400> 544

aagattcgct tccatcaaca tcaat 25

<210> 545

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_5791\_13\_Forward\_Primer

<400> 545

aaagagagat tagggaacca ttgga 25

<210> 546

<211> 26

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_5791\_13\_Reverse\_Primer  
  
 <400> 546  
  
 aatccaaata gaaatttcgt gtcagt 26  
  
  
 <210> 547  
 <211> 20  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_206841\_19\_Forward\_Primer  
  
 <400> 547  
  
 agctgcctca caccgccaat 20  
  
  
 <210> 548  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_206841\_19\_Reverse\_Primer  
  
 <400> 548  
  
 actagcatct ctcggtccct cactt 25  
  
  
 <210> 549  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_202827\_12\_Forward\_Primer  
  
 <400> 549  
  
 agttggctca aacaaatcag attcc 25  
  
  
 <210> 550  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_202827\_12\_Reverse\_Primer  
  
 <400> 550  
  
 tgtaggaga agaaccacca ccaag 25

<210> 551  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_322656\_13\_Forward\_Primer  
  
 <400> 551  
  
 tgtccaata tcctaggtag agccata 27  
  
  
 <210> 552  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_322656\_13\_Reverse\_Primer  
  
 <400> 552  
  
 cggtttgatc acattcactt gtcac 25  
  
  
 <210> 553  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_111841\_14\_Forward\_Primer  
  
 <400> 553  
  
 tgctttagct cagtaacctg cttga 25  
  
  
 <210> 554  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_111841\_14\_Reverse\_Primer  
  
 <400> 554  
  
 catgttagtt tatcttgctg gcatcc 26  
  
  
 <210> 555  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_192719\_13\_Forward\_Primer  
  
 <400> 555  
  
 gctacttctt ggcaagctct attcg 25

<210> 556  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_192719\_13\_Reverse\_Primer  
  
 <400> 556  
  
 gttgttgtgc ctttagggtc aatgt 25  
  
 <210> 557  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_195630\_17\_Forward\_Primer  
  
 <400> 557  
  
 ttggagttga gtgttctgat ggaag 25  
  
 <210> 558  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_195630\_17\_Reverse\_Primer  
  
 <400> 558  
  
 tctctcgtac gatgacccta atgaa 25  
  
 <210> 559  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_69999\_13\_Forward\_Primer  
  
 <400> 559  
  
 tttccacaaa gactcctgcc cttt 24  
  
 <210> 560  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_69999\_13\_Reverse\_Primer  
  
 <400> 560

tagtgacaca gtgtggtgga gtgaa 25

<210> 561

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_11176\_13\_Forward\_Primer

<400> 561

cgttctcgtc gaataatacc gattc 25

<210> 562

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_11176\_13\_Reverse\_Primer

<400> 562

accaataaga ttgccttacg aattt 25

<210> 563

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_228643\_13\_Forward\_Primer

<400> 563

gctatagcag ctaggaactg gtgga 25

<210> 564

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_228643\_13\_Reverse\_Primer

<400> 564

attgatcatc agagcatgaa cttcg 25

<210> 565

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_88478\_19\_Forward\_Primer

<400> 565  
aagataagat gaggtgctcg tcaaa 25

<210> 566  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_88478\_19\_Reverse\_Primer

<400> 566  
ttataactcat tcaatgcacg attgg 25

<210> 567  
<211> 21  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_108950\_13\_Forward\_Primer

<400> 567  
agtgctagct ggacgcacaa a 21

<210> 568  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_108950\_13\_Reverse\_Primer

<400> 568  
aaactggaat caatcatcaa atgtgt 26

<210> 569  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_121054\_14\_Forward\_Primer

<400> 569  
ctgcatggaa agatgaagca ggtat 25

<210> 570  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_121054\_14\_Reverse\_Primer  
<400> 570  
gtgctttctc cctggcagac tataa 25  
  
<210> 571  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_188337\_14\_Forward\_Primer  
<400> 571  
cacgtaagac caagacctaa cagga 25  
  
<210> 572  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_188337\_14\_Reverse\_Primer  
<400> 572  
attcaagact gtgcatcttc ttcgt 25  
  
<210> 573  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_255944\_21\_Forward\_Primer  
<400> 573  
taactttgcc ttaattgggt gcaca 25  
  
<210> 574  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_255944\_21\_Reverse\_Primer  
<400> 574  
attcttcttg ccttctcact gccta 25  
  
<210> 575  
<211> 25



<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_219518\_14\_Forward\_Primer  
  
<400> 575  
  
acgaaatgct catgatcttc ttcca 25  
  
<210> 576  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_219518\_14\_Reverse\_Primer  
  
<400> 576  
  
aatctgcagg agagagaaag cgtaa 25  
  
<210> 577  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_235601\_15\_Forward\_Primer  
  
<400> 577  
  
acactcagtc atagccaagc ctacc 25  
  
<210> 578  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_235601\_15\_Reverse\_Primer  
  
<400> 578  
  
tgagttggac gaggacaagg taagt 25  
  
<210> 579  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_301529\_13\_Forward\_Primer  
  
<400> 579  
  
ttagttttaca ctgccggatc acgtt 25

<210> 580  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_301529\_13\_Reverse\_Primer  
  
 <400> 580  
  
 gagcagtcta atccattgga aatca 25  
  
 <210> 581  
 <211> 22  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_94795\_14\_Forward\_Primer  
  
 <400> 581  
  
 ccgtctccaa caccctctca ta 22  
  
 <210> 582  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_94795\_14\_Reverse\_Primer  
  
 <400> 582  
  
 tccaactgaa gagaagaagg cattg 25  
  
 <210> 583  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_46703\_23\_Forward\_Primer  
  
 <400> 583  
  
 aaaccattct tcaacttgca acaca 25  
  
 <210> 584  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_46703\_23\_Reverse\_Primer  
  
 <400> 584

tcttcttgtc agaaacacgg ttgaa 25

<210> 585  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_59616\_14\_Forward\_Primer

<400> 585

tcatggtaac atggaggcaa ctatc 25

<210> 586  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_59616\_14\_Reverse\_Primer

<400> 586

ccctaaatca tcaccatcat cactt 25

<210> 587  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_296933\_15\_Forward\_Primer

<400> 587

ttagtggaaa caagcactct ctcct 25

<210> 588  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_296933\_15\_Reverse\_Primer

<400> 588

ttctatgctc ttgccaccaa atgta 25

<210> 589  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_192428\_17\_Forward\_Primer

<400> 589  
ataacagcga agcaatccat taacc 25

<210> 590  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_192428\_17\_Reverse\_Primer

<400> 590  
cgaatagagc ttgccaagaa gtagc 25

<210> 591  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_191490\_14\_Forward\_Primer

<400> 591  
gcataataca ttgtgtcttc atcca 25

<210> 592  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_191490\_14\_Reverse\_Primer

<400> 592  
attcaagact gtgcatcttc ttcgt 25

<210> 593  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_201115\_11\_Forward\_Primer

<400> 593  
tctcattgat ccttgtccat ccata 25

<210> 594  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_201115\_11\_Reverse\_Primer  
 <400> 594  
 tgcacaacta ctaataccat cgtcca 26  
  
 <210> 595  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_72882\_15\_Forward\_Primer  
 <400> 595  
 tgatcaccac agtaatatca atcaca 27  
  
 <210> 596  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_72882\_15\_Reverse\_Primer  
 <400> 596  
 ggtaatttaa tgttcacaca tgaccac 27  
  
 <210> 597  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_69514\_13\_Forward\_Primer  
 <400> 597  
 aaactttgca tcacattggt aatcttt 27  
  
 <210> 598  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_69514\_13\_Reverse\_Primer  
 <400> 598  
 aatccaccta cacgaatttg ctcac 25  
  
 <210> 599  
 <211> 25  
 <212> DNA

<213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_37699\_47\_Forward\_Primer  
 <400> 599  
 gtggaatcaa gtgagggaga aactc 25  
  
 <210> 600  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_37699\_47\_Reverse\_Primer  
 <400> 600  
 tctcttcttt cttaatcgcc taatca 26  
  
 <210> 601  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_11301\_29\_Forward\_Primer  
 <400> 601  
 ccatttatac acacacacac acacaca 27  
  
 <210> 602  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_11301\_29\_Reverse\_Primer  
 <400> 602  
 tcacgtagat ttcacacttc ctcaa 25  
  
 <210> 603  
 <211> 22  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_141875\_12\_Forward\_Primer  
 <400> 603  
 gctcatgatt cgggcatat tt 22  
  
 <210> 604

<211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_141875\_12\_Reverse\_Primer  
  
 <400> 604  
  
 tgagcaaatt gttgtgttga gtagtg 26  
  
 <210> 605  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_98090\_18\_Forward\_Primer  
  
 <400> 605  
  
 aaacacacac tgaacttggt cctaaa 26  
  
 <210> 606  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_98090\_18\_Reverse\_Primer  
  
 <400> 606  
  
 acatatgcag tacaatccgc agaag 25  
  
 <210> 607  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_43298\_35\_Forward\_Primer  
  
 <400> 607  
  
 tggttcata agactctcga acaaa 25  
  
 <210> 608  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_43298\_35\_Reverse\_Primer  
  
 <400> 608  
  
 acatgtatca cgggtgaaca acatt 25

<210> 609  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_262094\_11\_Forward\_Primer  
  
<400> 609  
  
ggatccaacc gactagatca gtctaa 26  
  
<210> 610  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_262094\_11\_Reverse\_Primer  
  
<400> 610  
  
ttctaatagac actttgtgaa tgaagg 26  
  
<210> 611  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_262079\_15\_Forward\_Primer  
  
<400> 611  
  
ggatccaacc gactagatca gtctaa 26  
  
<210> 612  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_262079\_15\_Reverse\_Primer  
  
<400> 612  
  
ttctaatagac actttgtgaa tgaagg 26  
  
<210> 613  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_59090\_12\_Forward\_Primer  
  
<400> 613



tctcatttat ctatctccca aggtgtg 27

<210> 614

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_59090\_12\_Reverse\_Primer

<400> 614

cctaacaccg tgcctaagga cataa 25

<210> 615

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_245723\_13\_Forward\_Primer

<400> 615

aacgttgatg tctactgctc ccaat 25

<210> 616

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_245723\_13\_Reverse\_Primer

<400> 616

gcgcgtggat aataattggtt tgttt 25

<210> 617

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_194628\_54\_Forward\_Primer

<400> 617

gattaggcac ccataatata aatcctt 27

<210> 618

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_194628\_54\_Reverse\_Primer

<400> 618  
atgttaccaa ctccgacacg tcagt 25

<210> 619  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_4566\_16\_Forward\_Primer

<400> 619  
ccaaacacct cctcaattgt agacc 25

<210> 620  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_4566\_16\_Reverse\_Primer

<400> 620  
tttcttgaag ttgcctgtg tactatc 27

<210> 621  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_96209\_14\_Forward\_Primer

<400> 621  
ttgatgagct ggctgggttag ttaaa 25

<210> 622  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_96209\_14\_Reverse\_Primer

<400> 622  
gtaatgtagg ctttcgctcc ctctt 25

<210> 623  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_\_248715\_17\_Forward\_Primer  
<400> 623  
agcaaagtct ttaattacgc tgaaa 25  
  
<210> 624  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_248715\_17\_Reverse\_Primer  
<400> 624  
ttcttgggtggt attgcttgct actcg 25  
  
<210> 625  
<211> 23  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_71410\_40\_Forward\_Primer  
<400> 625  
gagtccttca aattggcgctc ttt 23  
  
<210> 626  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_71410\_40\_Reverse\_Primer  
<400> 626  
aagtttggct agattcaaga aacaaa 26  
  
<210> 627  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 240017\_region\_G3\_\_226519\_13\_Forward\_Primer  
<400> 627  
ataatgcca cgatccaagt gtatt 25  
  
<210> 628  
<211> 25

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_226519\_13\_Reverse\_Primer  
  
 <400> 628  
  
 tccatttccg tactccaact ttcac 25  
  
  
 <210> 629  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_11282\_19\_Forward\_Primer  
  
 <400> 629  
  
 cgaaattcgt aaggcaatct tattgg 26  
  
  
 <210> 630  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_11282\_19\_Reverse\_Primer  
  
 <400> 630  
  
 tcacgtagat ttcacacttc ctcaa 25  
  
  
 <210> 631  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_170504\_12\_Forward\_Primer  
  
 <400> 631  
  
 aaccaaacct gggttgaact tgttt 25  
  
  
 <210> 632  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_170504\_12\_Reverse\_Primer  
  
 <400> 632  
  
 aaatgaaatc caaatcgggc cagt 24

<210> 633  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_40864\_14\_Forward\_Primer  
  
 <400> 633  
  
 ggactgattg gtacgaccat tagttta 27  
  
 <210> 634  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_40864\_14\_Reverse\_Primer  
  
 <400> 634  
  
 gcacatgaca aatcacatta ctctcaa 27  
  
 <210> 635  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_13529\_14\_Forward\_Primer  
  
 <400> 635  
  
 cgtgccaatc atcgatacag tacao 25  
  
 <210> 636  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_13529\_14\_Reverse\_Primer  
  
 <400> 636  
  
 cacaccacca gagtgttaagc tgttt 25  
  
 <210> 637  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_22858\_14\_Forward\_Primer  
  
 <400> 637  
  
 tcaattaaag ggataaggac ccatt 25

<210> 638  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_22858\_14\_Reverse\_Primer  
  
 <400> 638  
  
 ttttagagccc atttgtttca acttt 25  
  
 <210> 639  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_309211\_13\_Forward\_Primer  
  
 <400> 639  
  
 aaagttgaat ggtttgacag agataaa 27  
  
 <210> 640  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_309211\_13\_Reverse\_Primer  
  
 <400> 640  
  
 aaacactact gctgattatc ccaaga 26  
  
 <210> 641  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_55568\_26\_Forward\_Primer  
  
 <400> 641  
  
 aggcataaaa gcactaatgg tgaca 25  
  
 <210> 642  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 240017\_region\_G3\_\_55568\_26\_Reverse\_Primer  
  
 <400> 642

cctcctctct tgtaataggt cgatga 26

<210> 643  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_73238\_16\_Forward\_Primer  
 <400> 643

tggtcatgtg tgaacattaa attacct 27

<210> 644  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_73238\_16\_Reverse\_Primer  
 <400> 644

tcactccgtc tgtcccttat tacao 25

<210> 645  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_52488\_19\_Forward\_Primer  
 <400> 645

atgtgcattg gatgttctac catag 25

<210> 646  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 240017\_region\_G3\_\_52488\_19\_Reverse\_Primer  
 <400> 646

accaacaata cacaccgtac gtcac 25

<210> 647  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_471518\_14\_Forward\_Primer\_Seq

<400> 647  
 ttgcaactac ctgcaacgag gatac 25  
  
 <210> 648  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_471518\_14\_Reverse\_Primer\_Seq  
  
 <400> 648  
 aattatgtaa ttacgcgaga ttctcct 27  
  
 <210> 649  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231599\_23\_Forward\_Primer\_Seq  
  
 <400> 649  
 cttcaaggct ttggagaaca aacat 25  
  
 <210> 650  
 <211> 22  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231599\_23\_Reverse\_Primer\_Seq  
  
 <400> 650  
 aggtcctcgt actcctcctc ct 22  
  
 <210> 651  
 <211> 21  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_375912\_13\_Forward\_Primer\_Seq  
  
 <400> 651  
 gacgcatctg tcacgaacga c 21  
  
 <210> 652  
 <211> 23  
 <212> DNA  
 <213> Glycine max



<223> Seq ID: 318013\_region\_A3\_\_375912\_13\_Reverse\_Primer\_Seq  
<400> 652  
aaacctacgc cttcttcttc ctc 23  
  
<210> 653  
<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_180013\_12\_Forward\_Primer\_Seq  
<400> 653  
accagtactc ctggagggtc tcac 24  
  
<210> 654  
<211> 23  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_180013\_12\_Reverse\_Primer\_Seq  
<400> 654  
ctggtgctcc tgcaacatct tct 23  
  
<210> 655  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_171606\_14\_Forward\_Primer\_Seq  
<400> 655  
gcaactcgac atattctttg ggatt 25  
  
<210> 656  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_171606\_14\_Reverse\_Primer\_Seq  
<400> 656  
ctttccaatg tgggactgaa gaagt 25  
  
<210> 657  
<211> 24

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_416256\_13\_Forward\_Primer\_Seq  
  
 <400> 657  
  
 aacaattgca tccggtcatt ctaa 24  
  
  
 <210> 658  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_416256\_13\_Reverse\_Primer\_Seq  
  
 <400> 658  
  
 aattctcaca ctcaagaggc cagac 25  
  
  
 <210> 659  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231395\_15\_Forward\_Primer\_Seq  
  
 <400> 659  
  
 gtccttcccg cactaattta tcgaa 25  
  
  
 <210> 660  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231395\_15\_Reverse\_Primer\_Seq  
  
 <400> 660  
  
 gatcacccat caaacctac cttc 24  
  
  
 <210> 661  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_5502\_47Forward\_Primer\_Seq  
  
 <400> 661  
  
 cagcaagagt tgacgaatga tgaac 25

<210> 662  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_5502\_47\_Reverse\_Primer\_Seq  
  
 <400> 662  
  
 gctttaacac cgacaacctc atacc 25  
  
 <210> 663  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_93061\_14\_Forward\_Primer\_Seq  
  
 <400> 663  
  
 acagcatcag aactcagaag cattg 25  
  
 <210> 664  
 <211> 23  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_93061\_14\_Reverse\_Primer\_Seq  
  
 <400> 664  
  
 gaggctaacg ttgttgctga cct 23  
  
 <210> 665  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_111684\_19\_Forward\_Primer\_Seq  
  
 <400> 665  
  
 cttctccata acacttccca ccaac 25  
  
 <210> 666  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_111684\_19\_Reverse\_Primer\_Seq  
  
 <400> 666  
  
 tcgtgaggag aaggaagaga gaaag 25

<210> 667  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_69328\_14\_Forward\_Primer\_Seq  
  
 <400> 667  
  
 ctcttcagcc aggttacgct tatt 24  
  
 <210> 668  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_69328\_14\_Reverse\_Primer\_Seq  
  
 <400> 668  
  
 ccaaacgcga gagagaaata aagaa 25  
  
 <210> 669  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_36529\_17\_Forward\_Primer\_Seq  
  
 <400> 669  
  
 tcagagactt ctttgcttgg atgaa 25  
  
 <210> 670  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_36529\_17\_Reverse\_Primer\_Seq  
  
 <400> 670  
  
 caactacagg aaacgatgca aacaa 25  
  
 <210> 671  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_139128\_12\_Forward\_Primer\_Seq  
  
 <400> 671

cagttcggcg atatctgatt ctacc 25

<210> 672

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_139128\_12\_Reverse\_Primer\_Seq

<400> 672

ccagtgaagt tcttgaacct tgtca 25

<210> 673

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_495674\_13\_Forward\_Primer\_Seq

<400> 673

aagaatccag gaccatgacc ctatt 25

<210> 674

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_495674\_13\_Reverse\_Primer\_Seq

<400> 674

tttgcggtca ttctctgatg ttatt 25

<210> 675

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187577\_13\_Forward\_Primer\_Seq

<400> 675

aaacgaacac atacgcactc acatt 25

<210> 676

<211> 24

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187577\_13\_Reverse\_Primer\_Seq

<400> 676  
cttactggat ccatgaacgg tgga 24

<210> 677  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453036\_14\_Forward\_Primer\_Seq

<400> 677  
caacaatccg tgttgataag agcaa 25

<210> 678  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453036\_14\_Reverse\_Primer\_Seq

<400> 678  
ccctaaagca cttctagtcc cgaaa 25

<210> 679  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_374041\_13\_Forward\_Primer\_Seq

<400> 679  
aatgcaaagt aacaaagcac cctgt 25

<210> 680  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_374041\_13\_Reverse\_Primer\_Seq

<400> 680  
tttgttccac catgaataat gacca 25

<210> 681  
<211> 23  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_3412\_11\_\_Forward\_Primer\_Seq  
 <400> 681  
 aaacactcca atgccaccat ctc 23  
  
 <210> 682  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_3412\_11\_\_Reverse\_Primer\_Seq  
 <400> 682  
 aaccttaacc aaagccaaca ccttt 25  
  
 <210> 683  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_276495\_28\_\_Forward\_Primer\_Seq  
 <400> 683  
 ctttcaagcc gcagggttag atac 24  
  
 <210> 684  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_276495\_28\_\_Reverse\_Primer\_Seq  
 <400> 684  
 agctgcaacg tgtagccaat tatta 25  
  
 <210> 685  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_151839\_17\_\_Forward\_Primer\_Seq  
 <400> 685  
 ccgcaatggt atctctctca gactt 25  
  
 <210> 686  
 <211> 25

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_151839\_17\_Reverse\_Primer\_Seq  
  
 <400> 686  
  
 caggaagagg aagaggagga agaag 25  
  
  
 <210> 687  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_292912\_12\_Forward\_Primer\_Seq  
  
 <400> 687  
  
 atatgtttgc gtttctgtgc ttgtg 25  
  
  
 <210> 688  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_292912\_12\_Reverse\_Primer\_Seq  
  
 <400> 688  
  
 cccttaggaa tagagagaaa gagca 25  
  
  
 <210> 689  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_104560\_12\_Forward\_Primer\_Seq  
  
 <400> 689  
  
 aagagacaaa tggaggaaat tgcac 25  
  
  
 <210> 690  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_104560\_12\_Reverse\_Primer\_Seq  
  
 <400> 690  
  
 ccacttctcc aattcctctc tgaaa 25



<210> 691  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_65193\_11\_\_Forward\_Primer\_Seq  
  
<400> 691  
  
tagtggaatg gaagcagaac agagg 25  
  
<210> 692  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_65193\_11\_\_Reverse\_Primer\_Seq  
  
<400> 692  
  
tatgctgttc ttccaaacca ggagt 25  
  
<210> 693  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_110573\_70\_\_Forward\_Primer\_Seq  
  
<400> 693  
  
cacattgaaa taaacatgta cgacaca 27  
  
<210> 694  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_110573\_70\_\_Reverse\_Primer\_Seq  
  
<400> 694  
  
cgctggatat aatatttatg tgtgctg 27  
  
<210> 695  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_65117\_12\_\_Forward\_Primer\_Seq  
  
<400> 695  
  
tgcagtgtga gttcttcttt gatcc 25

<210> 696  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_65117\_12\_Reverse\_Primer\_Seq  
  
 <400> 696  
  
 tctgttctgc ttccattcca ctaaa 25  
  
 <210> 697  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_490837\_16\_Forward\_Primer\_Seq  
  
 <400> 697  
  
 agagaacgaa cggtagcatt ctcag 25  
  
 <210> 698  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_490837\_16\_Reverse\_Primer\_Seq  
  
 <400> 698  
  
 acatgcattg tgtgttgact ttcct 25  
  
 <210> 699  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_107448\_11\_Forward\_Primer\_Seq  
  
 <400> 699  
  
 tcagaaagtt tccctacttg attgagg 27  
  
 <210> 700  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_107448\_11\_Reverse\_Primer\_Seq  
  
 <400> 700

tccttcgatc aatttctggt ttgat 25

<210> 701  
 <211> 26  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_331\_23\_Forward\_Primer\_Seq

<400> 701

ccattgtcca tcctctctaa tgtttc 26

<210> 702  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_331\_23\_Reverse\_Primer\_Seq

<400> 702

tttcacatgt ccagtgttg attta 25

<210> 703  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_193470\_13\_Forward\_Primer\_Seq

<400> 703

taggcatagc ttaaggcatg gtatt 25

<210> 704  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_193470\_13\_Reverse\_Primer\_Seq

<400> 704

cctcatgtcc ttctgcttc tcata 25

<210> 705  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_183305\_14\_Forward\_Primer\_Seq

<400> 705  
ggagattaat ttgatgaacc gacca 25

<210> 706  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_183305\_14\_Reverse\_Primer\_Seq

<400> 706  
acagggtgag accaacacaa agatt 25

<210> 707  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_55050\_14\_Forward\_Primer\_Seq

<400> 707  
tctgaccctt aataatcagg caaca 25

<210> 708  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_55050\_14\_Reverse\_Primer\_Seq

<400> 708  
agaatcttct acttgcccg ttaga 25

<210> 709  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_224693\_21\_Forward\_Primer\_Seq

<400> 709  
tggtgctaag aaagtgaat ttgtgga 27

<210> 710  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_224693\_21\_Reverse\_Primer\_Seq  
 <400> 710  
 tttctttcaa acatgtggtg taccg 25  
  
 <210> 711  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_207216\_12\_Forward\_Primer\_Seq  
 <400> 711  
 ttaactttgt tagaggaggc ggaga 25  
  
 <210> 712  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_207216\_12\_Reverse\_Primer\_Seq  
 <400> 712  
 ctggctcggt gtcttcttca tgtt 24  
  
 <210> 713  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_4654\_22\_Forward\_Primer\_Seq  
 <400> 713  
 ctgaagaaag cattgaccaa ggaaa 25  
  
 <210> 714  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_4654\_22\_Reverse\_Primer\_Seq  
 <400> 714  
 aacctatctt aaccacaat cacag 25  
  
 <210> 715  
 <211> 25

<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_408959\_13\_Forward\_Primer\_Seq

<400> 715

cggttggttg aagaagttgt tgtta 25

<210> 716  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_408959\_13\_Reverse\_Primer\_Seq

<400> 716

gtgtagttag cgtggctctgc ttgtg 25

<210> 717  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_132288\_22\_Forward\_Primer\_Seq

<400> 717

acaggtcatc taaccaattg catgt 25

<210> 718  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_132288\_22\_Reverse\_Primer\_Seq

<400> 718

gttgcttatg tcttggacac cattg 25

<210> 719  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292822\_20\_Forward\_Primer\_Seq

<400> 719

gctattcaca aagcaagagc cgtta 25

<210> 720  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_292822\_20\_Reverse\_Primer\_Seq  
  
 <400> 720  
  
 agcacagaaa cgcaaacata taccc 25  
  
 <210> 721  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_311076\_12\_Forward\_Primer\_Seq  
  
 <400> 721  
  
 tttgtacttc gcacacattt gaagg 25  
  
 <210> 722  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_311076\_12\_Reverse\_Primer\_Seq  
  
 <400> 722  
  
 tttcctctcc tacccaaggt gagt 24  
  
 <210> 723  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_509623\_13\_Forward\_Primer\_Seq  
  
 <400> 723  
  
 aatgagcata gcgaagcctc ctaaa 25  
  
 <210> 724  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_509623\_13\_Reverse\_Primer\_Seq  
  
 <400> 724  
  
 tcgatggaaa ccctagatct cactc 25

<210> 725  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_190404\_14\_Forward\_Primer\_Seq  
  
 <400> 725  
  
 aatctggtcc ctcaaagaac aagtg 25  
  
 <210> 726  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_190404\_14\_Reverse\_Primer\_Seq  
  
 <400> 726  
  
 tttcccttat gcaagaagtt tgggtg 25  
  
 <210> 727  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_164916\_15\_Forward\_Primer\_Seq  
  
 <400> 727  
  
 aggctacggt atagaccacg ttgaa 25  
  
 <210> 728  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_164916\_15\_Reverse\_Primer\_Seq  
  
 <400> 728  
  
 gaatggaatt gatctttcca gaacc 25  
  
 <210> 729  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_21028\_13\_Forward\_Primer\_Seq  
  
 <400> 729



gatggataat tagtcttggc catcat 26

<210> 730

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_21028\_13\_Reverse\_Primer\_Seq

<400> 730

tattcctttg agcaagcaac tttga 25

<210> 731

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_208012\_17\_Forward\_Primer\_Seq

<400> 731

gttacaacag ctacctccgc agact 25

<210> 732

<211> 20

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_208012\_17\_Reverse\_Primer\_Seq

<400> 732

agtggcggac ctgattctcc 20

<210> 733

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_484089\_14\_Forward\_Primer\_Seq

<400> 733

cgatcgcatg atagagttca ccaat 25

<210> 734

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_484089\_14\_Reverse\_Primer\_Seq

<400> 734  
 actacgatgg cctctcctac gtttc 25  
  
 <210> 735  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318O13\_region\_A3\_\_332780\_17\_Forward\_Primer\_Seq  
  
 <400> 735  
 gttacaacag ctacctccgc agact 25  
  
 <210> 736  
 <211> 20  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318O13\_region\_A3\_\_332780\_17\_Reverse\_Primer\_Seq  
  
 <400> 736  
 agtggcggac ctgattctcc 20  
  
 <210> 737  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318O13\_region\_A3\_\_480137\_37\_Forward\_Primer\_Seq  
  
 <400> 737  
 ttcaagggaa ggagaagaat agattt 26  
  
 <210> 738  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318O13\_region\_A3\_\_480137\_37\_Reverse\_Primer\_Seq  
  
 <400> 738  
 tccctattaa gtttccttta atccatc 27  
  
 <210> 739  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_441056\_14\_Forward\_Primer\_Seq  
<400> 739  
ctaatttgcg aacaggccac aagta 25

<210> 740  
<211> 24  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_441056\_14\_Reverse\_Primer\_Seq  
<400> 740  
gattacgaaa tttcttggcg gaag 24

<210> 741  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_77486\_11\_Forward\_Primer\_Seq  
<400> 741  
atacccaaat cccatcttcc atttc 25

<210> 742  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_77486\_11\_Reverse\_Primer\_Seq  
<400> 742  
gttgtgagca gaactaggag ccatt 25

<210> 743  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_272468\_11\_Forward\_Primer\_Seq  
<400> 743  
attggatcca tcctataagg caggt 25

<210> 744  
<211> 25

<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_272468\_11\_Reverse\_Primer\_Seq

<400> 744

ttgtacgttg catcagtaac acgaa 25

<210> 745  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_425319\_17\_Forward\_Primer\_Seq

<400> 745

taccagtgaaggatgagggtg actgt 25

<210> 746  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_425319\_17\_Reverse\_Primer\_Seq

<400> 746

tgaagcatac taagggcgta tccat 25

<210> 747  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_413879\_31\_Forward\_Primer\_Seq

<400> 747

gacccctcagc cttagtttgc tgaga 25

<210> 748  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_413879\_31\_Reverse\_Primer\_Seq

<400> 748

tgtcctgtaa tctgtcacca taggc 25

<210> 749  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_80477\_64\_Forward\_Primer\_Seq

<400> 749

ggttggcctg aataatttgc aatag 25

<210> 750  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_80477\_64\_Reverse\_Primer\_Seq

<400> 750

gggaagtggg atagttgata gcaga 25

<210> 751  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_277272\_50\_Forward\_Primer\_Seq

<400> 751

cctgatggta ctgcgttctc tctct 25

<210> 752  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_277272\_50\_Reverse\_Primer\_Seq

<400> 752

tctgtcattg aacatgcaca acatt 25

<210> 753  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_509642\_13\_Forward\_Primer\_Seq

<400> 753

ctaaacgctt tggtttcttc accac 25

<210> 754  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_509642\_13\_Reverse\_Primer\_Seq  
  
 <400> 754  
  
 tcgatcaata tcctctctcc gaatc 25  
  
 <210> 755  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_321771\_14\_Forward\_Primer\_Seq  
  
 <400> 755  
  
 atcaaactct ggaaacaggt tgggtg 25  
  
 <210> 756  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_321771\_14\_Reverse\_Primer\_Seq  
  
 <400> 756  
  
 gtcagcaaca ccttgggaatt aatgg 25  
  
 <210> 757  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_26788\_12\_Forward\_Primer\_Seq  
  
 <400> 757  
  
 gaagagacaa ttgtgaggca aatca 25  
  
 <210> 758  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_26788\_12\_Reverse\_Primer\_Seq  
  
 <400> 758

cagaccaatc atggttctct gctta 25

<210> 759

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_262706\_16\_Forward\_Primer\_Seq

<400> 759

ttccttatca cccaacatcc aaact 25

<210> 760

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_262706\_16\_Reverse\_Primer\_Seq

<400> 760

acactaggag tgcgggaaat aaatg 25

<210> 761

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_243928\_16\_Forward\_Primer\_Seq

<400> 761

tggcatgtga aacctaaata aacaa 25

<210> 762

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_243928\_16\_Reverse\_Primer\_Seq

<400> 762

tatcagggta tgcctgggaa gataa 25

<210> 763

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_23246\_148\_Forward\_Primer\_Seq

<400> 763  
aatcaccttt ctctgtccac ctctg 25

<210> 764  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_23246\_148\_Reverse\_Primer\_Seq

<400> 764  
aaggctcaaa tttgtaagcc aatca 25

<210> 765  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_165406\_12\_Forward\_Primer\_Seq

<400> 765  
ggcactgagc tgaattgtaa tgttg 25

<210> 766  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_165406\_12\_Reverse\_Primer\_Seq

<400> 766  
ccttgatgat ctctttaacc ctaag 25

<210> 767  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_486294\_14\_Forward\_Primer\_Seq

<400> 767  
cttatggcca tgctatacac atgct 25

<210> 768  
<211> 25  
<212> DNA  
<213> Glycine max



<223> Seq ID: 318013\_region\_A3\_\_486294\_14\_Reverse\_Primer\_Seq  
<400> 768  
actgaagtgc tttccatgat ccatt 25

<210> 769  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_46754\_12\_Forward\_Primer\_Seq  
<400> 769  
aatccaaagt tgtcaagatg gttcc 25

<210> 770  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_46754\_12\_Reverse\_Primer\_Seq  
<400> 770  
tcattgtcgg atcgttagat ttgaa 25

<210> 771  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381116\_15\_Forward\_Primer\_Seq  
<400> 771  
aaaggtgggt gtgcttccca tttat 25

<210> 772  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381116\_15\_Reverse\_Primer\_Seq  
<400> 772  
ccattcattc tcagatgctc catta 25

<210> 773  
<211> 25

<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350369\_11\_Forward\_Primer\_Seq

<400> 773

aaaggttgaa gaagatgctg cgtaa 25

<210> 774  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350369\_11\_Reverse\_Primer\_Seq

<400> 774

tcacgttgaa cggtttgaaa tactc 25

<210> 775  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_138841\_13\_Forward\_Primer\_Seq

<400> 775

ggtgcagctt aaacaatttc tgtca 25

<210> 776  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_138841\_13\_Reverse\_Primer\_Seq

<400> 776

tttgaatacg ttggagagct tggat 25

<210> 777  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_12158\_142\_Forward\_Primer\_Seq

<400> 777

catacccttt cagagtcctt gtcac 25

<210> 778  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318O13\_region\_A3\_\_12158\_142\_Reverse\_Primer\_Seq  
  
<400> 778  
  
tggaggaagt atgaaattcg tttcg 25  
  
<210> 779  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318O13\_region\_A3\_\_315368\_13\_Forward\_Primer\_Seq  
  
<400> 779  
  
cagtcagaga aaggaagcat gcact 25  
  
<210> 780  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318O13\_region\_A3\_\_315368\_13\_Reverse\_Primer\_Seq  
  
<400> 780  
  
ctggagcaaa ggatgaaagt gaagt 25  
  
<210> 781  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318O13\_region\_A3\_\_307549\_13\_Forward\_Primer\_Seq  
  
<400> 781  
  
ctggagcaaa ggatgaaagt gaagt 25  
  
<210> 782  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318O13\_region\_A3\_\_307549\_13\_Reverse\_Primer\_Seq  
  
<400> 782  
  
cagtcagaga aaggaagcat gcact 25

<210> 783  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_159857\_14\_Forward\_Primer\_Seq  
  
 <400> 783  
  
 tcctcctcct agttgtgctt ctctt 25  
  
 <210> 784  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_159857\_14\_Reverse\_Primer\_Seq  
  
 <400> 784  
  
 aaggatatgc tgaccgcaat ctaat 25  
  
 <210> 785  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_140551\_15\_Forward\_Primer\_Seq  
  
 <400> 785  
  
 gattcctggt tcttgaatt tcctt 25  
  
 <210> 786  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_140551\_15\_Reverse\_Primer\_Seq  
  
 <400> 786  
  
 caaacgcata ccagatgaca ataca 25  
  
 <210> 787  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_279869\_11\_Forward\_Primer\_Seq  
  
 <400> 787

taatgtgccca acttctagca aggat 25

<210> 788

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_279869\_11\_Reverse\_Primer\_Seq

<400> 788

agtctgggct tatggccaaa tttat 25

<210> 789

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_78292\_35\_Forward\_Primer\_Seq

<400> 789

caaattgatt agtttctttc cttctcc 27

<210> 790

<211> 26

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_78292\_35\_Reverse\_Primer\_Seq

<400> 790

catgttcttt catcaagaat caatgc 26

<210> 791

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_185019\_12\_Forward\_Primer\_Seq

<400> 791

aaccttctcg cgtagcttga gtaga 25

<210> 792

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_185019\_12\_Reverse\_Primer\_Seq  
<400> 792  
tcatgctcac caatgctctc ataat 25  
  
<210> 793  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_409164\_13\_Forward\_Primer\_Seq  
<400> 793  
aggagaaaca tcagcatcat tacgg 25  
  
<210> 794  
<211> 22  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_409164\_13\_Reverse\_Primer\_Seq  
<400> 794  
aaagggtggg tgcataaga aa 22  
  
<210> 795  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_75392\_14\_Forward\_Primer\_Seq  
<400> 795  
gaaggagcct catcattgac ctaag 25  
  
<210> 796  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_75392\_14\_Reverse\_Primer\_Seq  
<400> 796  
cgatgacatt gatggttgat atcgt 25  
  
<210> 797  
<211> 25  
<212> DNA

<213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_231320\_12\_Forward\_Primer\_Seq  
 <400> 797  
 ccctaacaat catttcaacg ccttt 25  
  
 <210> 798  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_231320\_12\_Reverse\_Primer\_Seq  
 <400> 798  
 gccacgaatc gctgataaat aaaga 25  
  
 <210> 799  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_381102\_14\_Forward\_Primer\_Seq  
 <400> 799  
 ggccactgag aaacatgttc gata 24  
  
 <210> 800  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_381102\_14\_Reverse\_Primer\_Seq  
 <400> 800  
 caaagttatc tttcctctgg aaacca 26  
  
 <210> 801  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_491826\_15\_Forward\_Primer\_Seq  
 <400> 801  
 cttgtggcga tggtcctctt taata 25  
  
 <210> 802

<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_491826\_15\_Reverse\_Primer\_Seq  
  
<400> 802  
  
gaccaatctt cacaatccca caaa 24  
  
<210> 803  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_56365\_21\_Forward\_Primer\_Seq  
  
<400> 803  
  
catgttctcc acaaggaaac agaga 25  
  
<210> 804  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_56365\_21\_Reverse\_Primer\_Seq  
  
<400> 804  
  
ccatgactac agtttcaggc acaac 25  
  
<210> 805  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_372628\_15\_Forward\_Primer\_Seq  
  
<400> 805  
  
aaaggaaatc tgaaatcctg tggaa 25  
  
<210> 806  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_372628\_15\_Reverse\_Primer\_Seq  
  
<400> 806  
  
gggttggttac ttggctgata gatgg 25



<210> 807  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_217037\_11\_Forward\_Primer\_Seq  
  
<400> 807  
  
ggatctcttc aacactgacc atcct 25  
  
<210> 808  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_217037\_11\_Reverse\_Primer\_Seq  
  
<400> 808  
  
cctacccact tcaagttcaa ctgtc 25  
  
<210> 809  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_302609\_11\_Forward\_Primer\_Seq  
  
<400> 809  
  
cctacccact tcaagttcaa ctgtc 25  
  
<210> 810  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_302609\_11\_Reverse\_Primer\_Seq  
  
<400> 810  
  
ggatctcttc aacactgacc atcct 25  
  
<210> 811  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_341804\_11\_Forward\_Primer\_Seq  
  
<400> 811

ggatctcttc aacactgacc atcct 25

<210> 812  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_341804\_11\_Reverse\_Primer\_Seq

<400> 812

cctacccact tcaagttcaa ctgtc 25

<210> 813  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_264929\_68\_Forward\_Primer\_Seq

<400> 813

agctaaagca aagggtgggtt tgtaa 25

<210> 814  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_264929\_68\_Reverse\_Primer\_Seq

<400> 814

gcgtgattgt tctttatgca ttggt 25

<210> 815  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_55499\_12\_Forward\_Primer\_Seq

<400> 815

ttgctgcaag gtttcactct aattg 25

<210> 816  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_55499\_12\_Reverse\_Primer\_Seq

<400> 816  
aagaattatg tcaatgctcc tagcc 25

<210> 817  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_295634\_14\_Forward\_Primer\_Seq

<400> 817  
taagttcgtt ggtttgcctt gattt 25

<210> 818  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_295634\_14\_Reverse\_Primer\_Seq

<400> 818  
tttgtcaaat ccgactcaat ttattt 26

<210> 819  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_269358\_15\_Forward\_Primer\_Seq

<400> 819  
ttcatgatgg ttaggtcttg tgcag 25

<210> 820  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_269358\_15\_Reverse\_Primer\_Seq

<400> 820  
gagtgtagtg catgatgtga ggcta 25

<210> 821  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_457009\_24\_Forward\_Primer\_Seq  
<400> 821  
tgctgccatt ggagaaagtt gttat 25

<210> 822  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_457009\_24\_Reverse\_Primer\_Seq  
<400> 822  
ggctttctatt ccctcaactc accat 25

<210> 823  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_176598\_14\_Forward\_Primer\_Seq  
<400> 823  
ttcactataa aggatccgtt cagca 25

<210> 824  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_176598\_14\_Reverse\_Primer\_Seq  
<400> 824  
tgttggtaaa gagtggcaac aagaa 25

<210> 825  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_278266\_12\_Forward\_Primer\_Seq  
<400> 825  
tcttaatggc caattgctga aagtt 25

<210> 826  
<211> 27  
<212> DNA

<213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_278266\_12\_Reverse\_Primer\_Seq  
 <400> 826  
 cccattaata taacaaagtc aacatgg 27  
  
 <210> 827  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_391810\_12\_Forward\_Primer\_Seq  
 <400> 827  
 aaggagggttg gaggaatca tcaag 25  
  
 <210> 828  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_391810\_12\_Reverse\_Primer\_Seq  
 <400> 828  
 cacttactgt gcacaatttg attctc 26  
  
 <210> 829  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_269485\_15\_Forward\_Primer\_Seq  
 <400> 829  
 agcctcacat catgcactac actct 25  
  
 <210> 830  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_269485\_15\_Reverse\_Primer\_Seq  
 <400> 830  
 tccctcactt atgacaccac tcatc 25  
  
 <210> 831

<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_359247\_17\_Foward\_Primer\_Seq  
  
<400> 831  
  
ggttgagaag gagagtttaa gggttg 26  
  
<210> 832  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_359247\_17\_Reverse\_Primer\_Seq  
  
<400> 832  
  
ttcactccca attgtcatat aaaca 25  
  
<210> 833  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_315094\_13\_Foward\_Primer\_Seq  
  
<400> 833  
  
tccatataat ggacaggata tctgaat 27  
  
<210> 834  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_315094\_13\_Reverse\_Primer\_Seq  
  
<400> 834  
  
aaatgtcacg aggaaattat ttgttt 26  
  
<210> 835  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_307823\_13\_Foward\_Primer\_Seq  
  
<400> 835  
  
aaatgtcacg aggaaattat ttgttt 26

<210> 836  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_307823\_13\_Reverse\_Primer\_Seq  
  
<400> 836  
  
tccatataat ggacaggata tctgaat 27  
  
<210> 837  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_248588\_15\_Forward\_Primer\_Seq  
  
<400> 837  
  
gtctgcaagc taacagtgtc agagg 25  
  
<210> 838  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_248588\_15\_Reverse\_Primer\_Seq  
  
<400> 838  
  
gaattccac ttagtcatta ccacga 26  
  
<210> 839  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_252426\_85\_Forward\_Primer\_Seq  
  
<400> 839  
  
tcaattcaat gataaagtcc ttgga 26  
  
<210> 840  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_252426\_85\_Reverse\_Primer\_Seq  
  
<400> 840

tggtttgctt aggtagaaca agaaat 26

<210> 841  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_513314\_16\_Forward\_Primer\_Seq

<400> 841

cttaaagtgc gttatcgtca gcgta 25

<210> 842  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_513314\_16\_Reverse\_Primer\_Seq

<400> 842

actgatactg accaaatgac catgc 25

<210> 843  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_68183\_14\_Forward\_Primer\_Seq

<400> 843

caccgtgaag atgatcaaga gagag 25

<210> 844  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_68183\_14\_Reverse\_Primer\_Seq

<400> 844

taggatagcc caccaacaag gataa 25

<210> 845  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_471191\_13\_Forward\_Primer\_Seq



<400> 845  
 cgtcacttga cctcaacaat gtgta 25

<210> 846  
 <211> 26  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_471191\_13\_Reverse\_Primer\_Seq

<400> 846  
 tgccaaatta atctcattat ggtacg 26

<210> 847  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_163547\_18\_Forward\_Primer\_Seq

<400> 847  
 tttgcaaatac atgcatccta agttt 25

<210> 848  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_163547\_18\_Reverse\_Primer\_Seq

<400> 848  
 tgaatgcaca agtgtatttg cagag 25

<210> 849  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_417867\_15\_Forward\_Primer\_Seq

<400> 849  
 gtttgggtct gaatctgaag aaacg 25

<210> 850  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_417867\_15\_Reverse\_Primer\_Seq  
<400> 850  
gcgaatctag cgtagttggt gaaat 25

<210> 851  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_332465\_14\_Forward\_Primer\_Seq  
<400> 851  
taacgctgca tgatttgagt tctgt 25

<210> 852  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_332465\_14\_Reverse\_Primer\_Seq  
<400> 852  
ttggactttg gagaccacat tcttt 25

<210> 853  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_207697\_14\_Forward\_Primer\_Seq  
<400> 853  
taacgctgca tgatttgagt tctgt 25

<210> 854  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_207697\_14\_Reverse\_Primer\_Seq  
<400> 854  
ttggactttg gagaccacat tcttt 25

<210> 855  
<211> 25  
<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_277229\_43\_Foward\_Primer\_Seq

<400> 855

caagccaaca tacacagtgg ttctg 25

<210> 856

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_277229\_43\_Reverse\_Primer\_Seq

<400> 856

tctgtcattg aacatgcaca acatt 25

<210> 857

<211> 23

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_36366\_11\_Foward\_Primer\_Seq

<400> 857

aattgtacgg cagacacgtc ctc 23

<210> 858

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_36366\_11\_Reverse\_Primer\_Seq

<400> 858

aaagaagtct ctgacttgcc tccac 25

<210> 859

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_91970\_12\_Foward\_Primer\_Seq

<400> 859

tcttttgaca ctgtgagagg tgttt 25

<210> 860

<211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_91970\_12\_Reverse\_Primer\_Seq  
  
 <400> 860  
  
 tccatgattc tattcgacct taacaa 26  
  
  
 <210> 861  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_211533\_11\_Forward\_Primer\_Seq  
  
 <400> 861  
  
 ggtgtgttgg gagagtcaac agtct 25  
  
  
 <210> 862  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_211533\_11\_Reverse\_Primer\_Seq  
  
 <400> 862  
  
 aaagggtatg aggggtgggaa tgaat 25  
  
  
 <210> 863  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_336301\_11\_Forward\_Primer\_Seq  
  
 <400> 863  
  
 ggtgtgttgg gagagtcaac agtct 25  
  
  
 <210> 864  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_336301\_11\_Reverse\_Primer\_Seq  
  
 <400> 864  
  
 aaagggtatg aggggtgggaa tgaat 25

<210> 865  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_441603\_14\_Forward\_Primer\_Seq  
  
 <400> 865  
  
 gtggtagtcc gcaatgagac aatct 25  
  
  
 <210> 866  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_441603\_14\_Reverse\_Primer\_Seq  
  
 <400> 866  
  
 aacatccatt ctcgaagacc aagtc 25  
  
  
 <210> 867  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_468354\_15\_Forward\_Primer\_Seq  
  
 <400> 867  
  
 tttcttactg cacctagtcc acgac 25  
  
  
 <210> 868  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_468354\_15\_Reverse\_Primer\_Seq  
  
 <400> 868  
  
 gcctgaataa tcggttaaag taccg 25  
  
  
 <210> 869  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_188983\_18\_Forward\_Primer\_Seq  
  
 <400> 869

tgcgaaattgg taacgatctt acttc 25

<210> 870  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_188983\_18\_Reverse\_Primer\_Seq

<400> 870

aattcatcta agttctgcga tgataaa 27

<210> 871  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_115502\_17\_Forward\_Primer\_Seq

<400> 871

gttattggtc ggtgtacctg atcgt 25

<210> 872  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_115502\_17\_Reverse\_Primer\_Seq

<400> 872

ggagagttga cacagatgca taacg 25

<210> 873  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_163006\_13\_Forward\_Primer\_Seq

<400> 873

tgatggtaat gaatcagatc aacga 25

<210> 874  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_163006\_13\_Reverse\_Primer\_Seq

<400> 874  
taaccacacg agattgcaac aaagt 25

<210> 875  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_119283\_14\_Forward\_Primer\_Seq

<400> 875  
tgaagtggag taaggtcttg ttgaa 26

<210> 876  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_119283\_14\_Reverse\_Primer\_Seq

<400> 876  
taaacatgca attgacagat gctga 25

<210> 877  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_491126\_11\_Forward\_Primer\_Seq

<400> 877  
cctctctacc aaacacaagc agaaa 25

<210> 878  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_491126\_11\_Reverse\_Primer\_Seq

<400> 878  
agctccactg gtaagtccaa ttcac 25

<210> 879  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_99512\_21\_\_Forward\_Primer\_Seq  
<400> 879  
tatatcgtgc atgtttgttg gctct 25  
  
<210> 880  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_99512\_21\_\_Reverse\_Primer\_Seq  
<400> 880  
caagtcacca cccaaggaag tatct 25  
  
<210> 881  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_280291\_17\_\_Forward\_Primer\_Seq  
<400> 881  
tgaaatccca actataggtt gacacc 26  
  
<210> 882  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_280291\_17\_\_Reverse\_Primer\_Seq  
<400> 882  
gggactttct cccaacattt cattt 25  
  
<210> 883  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_138443\_19\_\_Forward\_Primer\_Seq  
<400> 883  
tgataaagcc aaagaagtaa ctttcg 26  
  
<210> 884  
<211> 24  
<212> DNA



<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_138443\_19\_Reverse\_Primer\_Seq

<400> 884

ggttcatcac cttgtcacac ctct 24

<210> 885

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_115973\_14\_Forward\_Primer\_Seq

<400> 885

ttaagcaatt gagttggatg aggtg 25

<210> 886

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_115973\_14\_Reverse\_Primer\_Seq

<400> 886

atgattgttc aagtgggtgct tcctc 25

<210> 887

<211> 26

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_329977\_14\_Forward\_Primer\_Seq

<400> 887

cagagagtcg tgtttaagca tttgaa 26

<210> 888

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_329977\_14\_Reverse\_Primer\_Seq

<400> 888

ggaaagccga aggacatcta ttcta 25

<210> 889

<211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_205203\_14\_Forward\_Primer\_Seq  
  
 <400> 889  
  
 cagagagtcg tgtttaagca ttgaa 26  
  
  
 <210> 890  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_205203\_14\_Reverse\_Primer\_Seq  
  
 <400> 890  
  
 ggaaagccga aggacatcta ttcta 25  
  
  
 <210> 891  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_153114\_12\_Forward\_Primer\_Seq  
  
 <400> 891  
  
 agttacaact ttcgcatcgg ttaca 25  
  
  
 <210> 892  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_153114\_12\_Reverse\_Primer\_Seq  
  
 <400> 892  
  
 tgtcaggaga gggtttagga acaag 25  
  
  
 <210> 893  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_34581\_13\_Forward\_Primer\_Seq  
  
 <400> 893  
  
 gtacttgatc ccagacacca cttgc 25

<210> 894  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_34581\_13\_Reverse\_Primer\_Seq  
  
 <400> 894  
  
 cgacaccgta tacgtaactc cattg 25  
  
  
 <210> 895  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_292577\_19\_Forward\_Primer\_Seq  
  
 <400> 895  
  
 ccattgtagg aggacaagaa tcaca 25  
  
  
 <210> 896  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_292577\_19\_Reverse\_Primer\_Seq  
  
 <400> 896  
  
 agcaacaaca acaacacaga acaca 25  
  
  
 <210> 897  
 <211> 27  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_445391\_20\_Forward\_Primer\_Seq  
  
 <400> 897  
  
 tgcatttatc attgaattag agggatt 27  
  
  
 <210> 898  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_445391\_20\_Reverse\_Primer\_Seq  
  
 <400> 898

agcaaacgca atgcaataca gtaac 25

<210> 899  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350540\_17\_Forward\_Primer\_Seq

<400> 899

gggaagagta tttcaaaccg ttcaa 25

<210> 900  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_350540\_17\_Reverse\_Primer\_Seq

<400> 900

ttgagttaaa ttgtggttgc atggt 25

<210> 901  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453879\_15\_Forward\_Primer\_Seq

<400> 901

gcagcactga acatgataag agatca 26

<210> 902  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_453879\_15\_Reverse\_Primer\_Seq

<400> 902

tgcaattgaa gaacaagaaa ggaca 25

<210> 903  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_201246\_13\_Forward\_Primer\_Seq

<400> 903  
tgtgtggaat gcacatttag agaaga 26

<210> 904  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_201246\_13\_Reverse\_Primer\_Seq

<400> 904  
cgcaagatga tgttgattga tatgc 25

<210> 905  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_326020\_13\_Forward\_Primer\_Seq

<400> 905  
tgtgtggaat gcacatttag agaaga 26

<210> 906  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_326020\_13\_Reverse\_Primer\_Seq

<400> 906  
cgcaagatga tgttgattga tatgc 25

<210> 907  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_503801\_14\_Forward\_Primer\_Seq

<400> 907  
atttgcatto agtgtgaaca ttgct 25

<210> 908  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_503801\_14\_Reverse\_Primer\_Seq  
<400> 908  
tgggacttaa cataatctga ggaaaga 27

<210> 909  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_302400\_52\_Forward\_Primer\_Seq  
<400> 909  
tacataaaga accatgtgag gaagg 25

<210> 910  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_302400\_52\_Reverse\_Primer\_Seq  
<400> 910  
tgactgttga ttgatagcct tgttga 26

<210> 911  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_448857\_15\_Forward\_Primer\_Seq  
<400> 911  
atgaactggt gttcctgtca tgttg 25

<210> 912  
<211> 24  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_448857\_15\_Reverse\_Primer\_Seq  
<400> 912  
aaaccctcaa accaccttgg atac 24

<210> 913  
<211> 25  
<212> DNA

<213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_48364\_14\_Forward\_Primer\_Seq  
 <400> 913  
 aacaagtcac caaggcaciaa cttta 25  
  
 <210> 914  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_48364\_14\_Reverse\_Primer\_Seq  
 <400> 914  
 aagaccagag aacaagccaa ttcc 24  
  
 <210> 915  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_251804\_48\_Forward\_Primer\_Seq  
 <400> 915  
 tgttatcaat cgacgcaata atcaa 25  
  
 <210> 916  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_251804\_48\_Reverse\_Primer\_Seq  
 <400> 916  
 acgatgaggt gttgccattt atttc 25  
  
 <210> 917  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_382583\_13\_Forward\_Primer\_Seq  
 <400> 917  
 ccctctatca agtgtatcag ccctta 26  
  
 <210> 918

<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_382583\_13\_Reverse\_Primer\_Seq  
  
<400> 918  
  
aggaaagtac accatttcta tcagga 26  
  
<210> 919  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_124737\_14\_Forward\_Primer\_Seq  
  
<400> 919  
  
tccaattagt tgcagaaaca agcaa 25  
  
<210> 920  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_124737\_14\_Reverse\_Primer\_Seq  
  
<400> 920  
  
tagtcctctt tggtgccaat acaca 25  
  
<210> 921  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_124766\_13\_Forward\_Primer\_Seq  
  
<400> 921  
  
tccaattagt tgcagaaaca agcaa 25  
  
<210> 922  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_124766\_13\_Reverse\_Primer\_Seq  
  
<400> 922  
  
tagtcctctt tggtgccaat acaca 25



<210> 923  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_461351\_16\_Forward\_Primer\_Seq  
  
 <400> 923  
  
 gaatggtggt aggggtgaag caact 25  
  
 <210> 924  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_461351\_16\_Reverse\_Primer\_Seq  
  
 <400> 924  
  
 atagtaattt gttgaagggc agcaa 25  
  
 <210> 925  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_64953\_19\_Forward\_Primer\_Seq  
  
 <400> 925  
  
 caccttgaga aacttgaaac acttga 26  
  
 <210> 926  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_64953\_19\_Reverse\_Primer\_Seq  
  
 <400> 926  
  
 ctctttaaag ggctactgcc ctcat 25  
  
 <210> 927  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_366586\_13\_Forward\_Primer\_Seq  
  
 <400> 927

tgtccatgca ttaaagcaaa catct 25

<210> 928  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_366586\_13\_Reverse\_Primer\_Seq

<400> 928

gaatgcaaac atgcgttatt tgtct 25

<210> 929  
 <211> 26  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_46190\_15\_\_Forward\_Primer\_Seq

<400> 929

caaacctcca atcactaaat tgatcc 26

<210> 930  
 <211> 24  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_46190\_15\_Reverse\_Primer\_Seq

<400> 930

aagttcaggc taggccaagg taca 24

<210> 931  
 <211> 26  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_81016\_11\_\_Forward\_Primer\_Seq

<400> 931

cctcggccaa acataactag tctaac 26

<210> 932  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_81016\_11\_Reverse\_Primer\_Seq

<400> 932  
agccttgatt ccatcttggt tggta 25

<210> 933  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_134426\_14\_Forward\_Primer\_Seq

<400> 933  
ttacactatg ggtccgttcg gttat 25

<210> 934  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_134426\_14\_Reverse\_Primer\_Seq

<400> 934  
tgaaacataa tggaagatga tgatgg 26

<210> 935  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292724\_14\_Forward\_Primer\_Seq

<400> 935  
ccattgtagg aggacaagaa tcaca 25

<210> 936  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_292724\_14\_Reverse\_Primer\_Seq

<400> 936  
taacggctct tgctttgtga atagc 25

<210> 937  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187096\_17\_Forward\_Primer\_Seq  
<400> 937  
gtccagccaa atgcgtaaca tttat 25

<210> 938  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_187096\_17\_Reverse\_Primer\_Seq  
<400> 938  
catctagtat ttgtttaacg ccgaaa 26

<210> 939  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381693\_13\_Forward\_Primer\_Seq  
<400> 939  
ttgatgttat gattcaatgg tttgat 26

<210> 940  
<211> 23  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_381693\_13\_Reverse\_Primer\_Seq  
<400> 940  
aaataccgcg tatcaacttc acc 23

<210> 941  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_361286\_33\_Forward\_Primer\_Seq  
<400> 941  
actccagttg cattctcttc gtaaa 25

<210> 942  
<211> 26  
<212> DNA

<213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_361286\_33\_Reverse\_Primer\_Seq  
 <400> 942  
 tgaaatgtgt tctttgttgc ttaccc 26  
  
 <210> 943  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_482668\_14\_Forward\_Primer\_Seq  
 <400> 943  
 cgttttgttac ttcacacgca cacat 25  
  
 <210> 944  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_482668\_14\_Reverse\_Primer\_Seq  
 <400> 944  
 tcagacttac gtacaagtgt gccata 26  
  
 <210> 945  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_128002\_12\_Forward\_Primer\_Seq  
 <400> 945  
 cttgccaggg atcaaatcat aaaga 25  
  
 <210> 946  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
 <223> Seq ID: 318013\_region\_A3\_\_128002\_12\_Reverse\_Primer\_Seq  
 <400> 946  
 tgtaagcttg caggacaagg taactc 26  
  
 <210> 947

<211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_499270\_14\_Forward\_Primer\_Seq  
  
 <400> 947  
  
 cactgtgtaa gtgtcccttg catct 25  
  
  
 <210> 948  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_499270\_14\_Reverse\_Primer\_Seq  
  
 <400> 948  
  
 gggatttgaa tcagaagact cgttt 25  
  
  
 <210> 949  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231650\_12\_Forward\_Primer\_Seq  
  
 <400> 949  
  
 cttcaaggct ttggagaaca aacat 25  
  
  
 <210> 950  
 <211> 22  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_231650\_12\_Reverse\_Primer\_Seq  
  
 <400> 950  
  
 caccggaaac cttcctctca tc 22  
  
  
 <210> 951  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_199851\_13\_Forward\_Primer\_Seq  
  
 <400> 951  
  
 cggccatagt catatttatg cttcc 25

<210> 952  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_199851\_13\_Reverse\_Primer\_Seq  
  
<400> 952  
  
agggttccaa tcacgctatt agtga 25  
  
<210> 953  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_324629\_13\_Forward\_Primer\_Seq  
  
<400> 953  
  
cggccatagt catatztatg cttcc 25  
  
<210> 954  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_324629\_13\_Reverse\_Primer\_Seq  
  
<400> 954  
  
agggttccaa tcacgctatt agtga 25  
  
<210> 955  
<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_374190\_19\_Forward\_Primer\_Seq  
  
<400> 955  
  
agccaaggta aggcacacaa actt 24  
  
<210> 956  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_374190\_19\_Reverse\_Primer\_Seq  
  
<400> 956

tcattccaatc cggtgataat agaaa 25

<210> 957

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_460603\_13\_Forward\_Primer\_Seq

<400> 957

cacgcaacca ttcatgttac aaagt 25

<210> 958

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_460603\_13\_Reverse\_Primer\_Seq

<400> 958

gaggattgaa tactgcccaa gctaa 25

<210> 959

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_108681\_14\_Forward\_Primer\_Seq

<400> 959

aagagtgtga aattggtacg acagt 25

<210> 960

<211> 24

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_108681\_14\_Reverse\_Primer\_Seq

<400> 960

gttcatcaag atgcaagcac cata 24

<210> 961

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_459791\_47\_Forward\_Primer\_Seq



<400> 961  
tgcttatgtc agctacggtc aatct 25

<210> 962  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_459791\_47\_Reverse\_Primer\_Seq

<400> 962  
tccgaggcga gtaggtacct ctatt 25

<210> 963  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_4257\_20\_Forward\_Primer\_Seq

<400> 963  
tcccaacgca acagtaacgt aaata 25

<210> 964  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_4257\_20\_\_Reverse\_Primer\_Seq

<400> 964  
tgaaacttga atgtaaccac tcccta 26

<210> 965  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_238810\_14\_Forward\_Primer\_Seq

<400> 965  
caggtgttaa tactcctttc atttcaa 27

<210> 966  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_238810\_14\_Reverse\_Primer\_Seq  
<400> 966  
acatcgtttc tatccaatga tgacg 25

<210> 967  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245817\_14\_Forward\_Primer\_Seq  
<400> 967  
atcataaatt cattcaaaca catgct 26

<210> 968  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245817\_14\_Reverse\_Primer\_Seq  
<400> 968  
actaccattc tgcgtgttta gatca 25

<210> 969  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245956\_14\_Forward\_Primer\_Seq  
<400> 969  
atcataaatt cattcaaaca catgct 26

<210> 970  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_245956\_14\_Reverse\_Primer\_Seq  
<400> 970  
actaccattc tgcgtgttta gatca 25

<210> 971  
<211> 26  
<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74148\_14\_\_Forward\_Primer\_Seq

<400> 971

tgcatgcatg taaccagaaa taataa 26

<210> 972

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74148\_14\_\_Reverse\_Primer\_Seq

<400> 972

cacactgcaa gagtgtatga agaaa 25

<210> 973

<211> 26

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74089\_15\_\_Forward\_Primer\_Seq

<400> 973

tgcatgcatg taaccagaaa taataa 26

<210> 974

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_74089\_15\_\_Reverse\_Primer\_Seq

<400> 974

cacactgcaa gagtgtatga agaaa 25

<210> 975

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 318013\_region\_A3\_\_241686\_12\_\_Forward\_Primer\_Seq

<400> 975

tggatcaaat ggtacttgct aactg 25

<210> 976

<211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_241686\_12\_Reverse\_Primer\_Seq  
  
 <400> 976  
  
 ccatttgccc acattattaa catca 25  
  
 <210> 977  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_47476\_12\_\_Forward\_Primer\_Seq  
  
 <400> 977  
  
 tttgcagcaa catatctgga ctttc 25  
  
 <210> 978  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_47476\_127\_Reverse\_Primer\_Seq  
  
 <400> 978  
  
 gtgttccatt atgtgcccag gttt 24  
  
 <210> 979  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_164550\_12\_Foward\_Primer\_Seq  
  
 <400> 979  
  
 caacataatc ctaatctccc atgct 25  
  
 <210> 980  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3\_\_164550\_12\_Reverse\_Primer\_Seq  
  
 <400> 980  
  
 gacatatggt cctccgggaa taaa 24

<210> 981  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_101255\_15\_Forward\_Primer\_Seq  
  
<400> 981  
  
gcactaatta agcctgtttc aacctg 26  
  
<210> 982  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 318013\_region\_A3\_\_101255\_15\_Reverse\_Primer\_Seq  
  
<400> 982  
  
tcattggacta attaatgtg gtcattc 27  
  
<210> 983  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_16189\_11\_Forward\_Primer  
  
<400> 983  
  
ttccacaaat ccaaattcca aattc 25  
  
<210> 984  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_16189\_11\_Reverse\_Primer  
  
<400> 984  
  
tgagattcca taggaaatca aagca 25  
  
<210> 985  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_71925\_13\_Forward\_Primer  
  
<400> 985

tccgactttg tggctatata tgtgtg 26

<210> 986

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_71925\_13\_Reverse\_Primer

<400> 986

agttgtgccc gatgtacatt acaaa 25

<210> 987

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_4707\_12\_Forward\_Primer

<400> 987

caagatcaag cacccttggt tctct 25

<210> 988

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_4707\_12Reverse\_Primer

<400> 988

tttccattac agacagtagc gtgtaaa 27

<210> 989

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_118904\_18\_Forward\_Primer

<400> 989

tagctgcac acctctcagt ttctg 25

<210> 990

<211> 26

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_118904\_18\_Reverse\_Primer

<400> 990  
ttgtccttaa atgtagccct gatttc 26

<210> 991  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_13655\_17\_Forward\_Primer

<400> 991  
gagtcaattt ccttaaacc atcaca 26

<210> 992  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_13655\_17\_Reverse\_Primer

<400> 992  
aagctcctgt ggacttgata ctcaga 26

<210> 993  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_53900\_13\_Forward\_Primer

<400> 993  
atttcttcac atcgatcatcc caaac 25

<210> 994  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_53900\_13\_Reverse\_Primer

<400> 994  
atgtgcttgg tggaatgtaa ggatt 25

<210> 995  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_8079\_14\_Forward\_Primer  
<400> 995  
gtgagagtta agctgggaac ctttg 25

<210> 996  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_8079\_14\_Reverse\_Primer  
<400> 996  
gatctctgtc tctcttcctt cttgc 25

<210> 997  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_9969\_28\_Forward\_Primer  
<400> 997  
tcaccagaga cgcattatca gattc 25

<210> 998  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_9969\_28\_Reverse\_Primer  
<400> 998  
cgctaccagc tactgtttcc ttctc 25

<210> 999  
<211> 27  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_72308\_77\_Forward\_Primer  
<400> 999  
tttcttaaac agatcactgg tatgcaa 27

<210> 1000  
<211> 25



<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_72308\_77\_Reverse\_Primer  
  
 <400> 1000  
  
 cgctaccagc tactgtttcc ttctc 25  
  
  
 <210> 1001  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_99475\_19\_Forward\_Primer  
  
 <400> 1001  
  
 tgcacaatga gatttgaagt catgta 26  
  
  
 <210> 1002  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_99475\_19\_Reverse\_Primer  
  
 <400> 1002  
  
 ttgagtcagg aatcttcgat taccc 25  
  
  
 <210> 1003  
 <211> 24  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_118615\_18\_Forward\_Primer  
  
 <400> 1003  
  
 atcatggatc tgattccacc tgaa 24  
  
  
 <210> 1004  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_118615\_18\_Reverse\_Primer  
  
 <400> 1004  
  
 tgattgtatg tatgggcgct aagtt 25

<210> 1005  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_119001\_46\_Forward\_Primer  
  
<400> 1005  
  
tgaaatcagg gctacattta aggaca 26  
  
<210> 1006  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_119001\_46\_Reverse\_Primer  
  
<400> 1006  
  
aggcatttgg tcaacttgat tatgc 25  
  
<210> 1007  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_118958\_43\_Forward\_Primer  
  
<400> 1007  
  
tgaaatcagg gctacattta aggaca 26  
  
<210> 1008  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_118958\_43\_Reverse\_Primer  
  
<400> 1008  
  
aggcatttgg tcaacttgat tatgc 25  
  
<210> 1009  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_17197\_13\_Forward\_Primer  
  
<400> 1009  
  
cggagtcgga gtagtcgagt agaca 25

<210> 1010  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_17197\_13\_Reverse\_Primer  
  
 <400> 1010  
  
 cataataccg agtccgatga aacct 25  
  
 <210> 1011  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_105163\_29\_Forward\_Primer  
  
 <400> 1011  
  
 ttccaattcc ttagcctatc aaaca 25  
  
 <210> 1012  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_105163\_29\_Reverse\_Primer  
  
 <400> 1012  
  
 aacatttgta cctatgcatt cccatc 26  
  
 <210> 1013  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_111335\_13\_Forward\_Primer  
  
 <400> 1013  
  
 atacttaciaa tccgtcaggc agctc 25  
  
 <210> 1014  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_111335\_13\_Reverse\_Primer  
  
 <400> 1014

tcatgttatg agtttgcgct cttgt 25

<210> 1015

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_106396\_13\_Forward\_Primer

<400> 1015

ctgtcaaggg aggaaattgg tacag 25

<210> 1016

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_106396\_13\_Reverse\_Primer

<400> 1016

aacaactgcc agaagaaagt accag 25

<210> 1017

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_59229\_17\_Forward\_Primer

<400> 1017

gcttgtcagg agagaaatgt tgctt 25

<210> 1018

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_59229\_17\_Reverse\_Primer

<400> 1018

aattcagcaa atgaaacatg ggagt 25

<210> 1019

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_73795\_20\_Forward\_Primer

<400> 1019  
 tggcaacact taatttgac agata 25  
  
 <210> 1020  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_73795\_20\_Reverse\_Primer  
  
 <400> 1020  
 gggaagaata acaaattaaa cccttt 26  
  
 <210> 1021  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_85664\_20\_Forward\_Primer  
  
 <400> 1021  
 tgtcaatcaa taaccattga tctcct 26  
  
 <210> 1022  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_85664\_20\_Reverse\_Primer  
  
 <400> 1022  
 ttggtttcta tttacgggta ccaaa 25  
  
 <210> 1023  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_36921\_17\_Forward\_Primer  
  
 <400> 1023  
 ccgagaccca cttggtatta cttca 25  
  
 <210> 1024  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_36921\_17\_Reverse\_Primer  
 <400> 1024  
 aggagtgaga aattgcttct ccaa 25

<210> 1025  
 <211> 24  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_124150\_19\_Forward\_Primer  
 <400> 1025  
 aagtgggtgc acacagcatc tagg 24

<210> 1026  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_124150\_19\_Reverse\_Primer  
 <400> 1026  
 tcactgaaca ctgatttctg ccatt 25

<210> 1027  
 <211> 26  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_5089\_14\_Forward\_Primer  
 <400> 1027  
 tcatacctga aatatgggtg tcttca 26

<210> 1028  
 <211> 25  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_5089\_14\_Reverse\_Primer  
 <400> 1028  
 cataacaaga caggttgagg caaca 25

<210> 1029  
 <211> 24

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_58221\_15\_Forward\_Primer  
  
 <400> 1029  
  
 catttcaaag ggagagccat catc 24  
  
  
 <210> 1030  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_58221\_15\_Reverse\_Primer  
  
 <400> 1030  
  
 catggaaatg gagaaagcaa agaaa 25  
  
  
 <210> 1031  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_96139\_14\_Forward\_Primer  
  
 <400> 1031  
  
 ccctcaagcc aatgatagta actcc 25  
  
  
 <210> 1032  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_96139\_14\_Reverse\_Primer  
  
 <400> 1032  
  
 aactcgtcct atgctcaacc ttacg 25  
  
  
 <210> 1033  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_70595\_13\_Forward\_Primer  
  
 <400> 1033  
  
 ttgggaactg tacacatgcc ttaat 25

<210> 1034  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_70595\_13\_Reverse\_Primer  
  
<400> 1034  
  
tgtttggtggt atttcatttg gaattat 27  
  
<210> 1035  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_4340\_15\_Forward\_Primer  
  
<400> 1035  
  
aaatatgggt acatcatccg atacaa 26  
  
<210> 1036  
<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_4340\_15\_Reverse\_Primer  
  
<400> 1036  
  
tttggatatg agaaggaggg aagg 24  
  
<210> 1037  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_90417\_11\_Forward\_Primer  
  
<400> 1037  
  
aaactgcaaa cacaaattgc ctaaa 25  
  
<210> 1038  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_90417\_11\_Reverse\_Primer  
  
<400> 1038  
  
cctggtagcc tgtacttgac ttggt 25



<210> 1039  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_49711\_17\_Forward\_Primer  
  
 <400> 1039  
  
 caaagagagg cagaggaggt gatta 25  
  
 <210> 1040  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_49711\_17\_Reverse\_Primer  
  
 <400> 1040  
  
 tggttgtagc tgcttgcac ttgat 25  
  
 <210> 1041  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_63053\_13\_Forward\_Primer  
  
 <400> 1041  
  
 tgtgcataac tcgatctctt gatga 25  
  
 <210> 1042  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_63053\_13\_Reverse\_Primer  
  
 <400> 1042  
  
 tcttgctgca atctttacta acagca 26  
  
 <210> 1043  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_63076\_14\_Forward\_Primer  
  
 <400> 1043

tgtgcataac tcgatctctt gatga 25

<210> 1044

<211> 26

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_63076\_14\_Reverse\_Primer

<400> 1044

tcttgctgca atctttacta acagca 26

<210> 1045

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44442\_12\_Forward\_Primer

<400> 1045

aacgcgtctt tctttcttct tcaac 25

<210> 1046

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44442\_12\_Reverse\_Primer

<400> 1046

gcaacatggc tatatgaaac acctc 25

<210> 1047

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44422\_19\_Forward\_Primer

<400> 1047

aacgcgtctt tctttcttct tcaac 25

<210> 1048

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_44422\_19\_Reverse\_Primer

<400> 1048  
 gcaacatggc tatatgaaac acctc 25  
  
 <210> 1049  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_44158\_19\_Forward\_Primer  
  
 <400> 1049  
 tttcattacg tgcgtttgta caacta 26  
  
 <210> 1050  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_44158\_19\_Reverse\_Primer  
  
 <400> 1050  
 caggggtggat gatacgaata cgatac 26  
  
 <210> 1051  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_44141\_17\_Forward\_Primer  
  
 <400> 1051  
 tttcattacg tgcgtttgta caacta 26  
  
 <210> 1052  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_44141\_17\_Reverse\_Primer  
  
 <400> 1052  
 caggggtggat gatacgaata cgatac 26  
  
 <210> 1053  
 <211> 27  
 <212> DNA  
 <213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_90762\_17\_Forward\_Primer  
 <400> 1053  
 ccagagatat gattcaatac aaaggaa 27  
  
 <210> 1054  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_90762\_17\_Reverse\_Primer  
 <400> 1054  
 attacccctgt ggtaacggat tcaag 25  
  
 <210> 1055  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_106241\_14\_Forward\_Primer  
 <400> 1055  
 tagatagcta gccatgttgg catga 25  
  
 <210> 1056  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_106241\_14\_Reverse\_Primer  
 <400> 1056  
 tgtaccaatt tcctcccttg acagt 25  
  
 <210> 1057  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_109676\_12\_Forward\_Primer  
 <400> 1057  
 tcattgtcctt tgaggacttt ctcatt 26  
  
 <210> 1058  
 <211> 26

<212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_109676\_12\_Reverse\_Primer  
  
 <400> 1058  
  
 tcactgacac tgagtgatag ccattt 26  
  
  
 <210> 1059  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_86242\_14\_Forward\_Primer  
  
 <400> 1059  
  
 ccacaactcc gatttatccc ataac 25  
  
  
 <210> 1060  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_86242\_14\_Reverse\_Primer  
  
 <400> 1060  
  
 gcacaaagaa gaaatttgga gtttca 26  
  
  
 <210> 1061  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_83109\_12\_Forward\_Primer  
  
 <400> 1061  
  
 tcacccttta ggagatccta gacac 25  
  
  
 <210> 1062  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_83109\_12\_Reverse\_Primer  
  
 <400> 1062  
  
 ctcttgccaa tgattgaagg aagtc 25

<210> 1063  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_10461\_15\_Forward\_Primer  
  
 <400> 1063  
  
 ggctgtgtgt gagtgagagt gagag 25  
  
 <210> 1064  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_10461\_15\_Reverse\_Primer  
  
 <400> 1064  
  
 tgcaccctta ttcctcctaa tcatac 25  
  
 <210> 1065  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_67608\_15\_Forward\_Primer  
  
 <400> 1065  
  
 ggtgggtaga tccaatttca tggtaga 26  
  
 <210> 1066  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_67608\_15\_Reverse\_Primer  
  
 <400> 1066  
  
 tcctgtacag cacgtatccg tattt 25  
  
 <210> 1067  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_63275\_46\_Forward\_Primer  
  
 <400> 1067  
  
 tgctgttagt aaagattgca gcaaga 26

<210> 1068  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_63275\_46\_Reverse\_Primer  
  
 <400> 1068  
  
 tataactccgc tcctcaattc cttca 25  
  
 <210> 1069  
 <211> 26  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_62405\_14\_Forward\_Primer  
  
 <400> 1069  
  
 tgcatagaga gaaatagacg aggaaa 26  
  
 <210> 1070  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_62405\_14\_Reverse\_Primer  
  
 <400> 1070  
  
 atctctttcca aacggtccat aagtt 25  
  
 <210> 1071  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_33563\_12\_Forward\_Primer  
  
 <400> 1071  
  
 ccttaggtgc tcatacatcc aaaca 25  
  
 <210> 1072  
 <211> 25  
 <212> DNA  
 <213> Glycine max  
  
 <223> Seq ID: 515002\_region\_G2\_\_33563\_12\_Reverse\_Primer

<400> 1072  
tgattcatat acaacgcaag aaacg 25

<210> 1073  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_33146\_14\_Forward\_Primer

<400> 1073  
cgaaccctaa acatttcaaa ccaaa 25

<210> 1074  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_33146\_14\_Reverse\_Primer

<400> 1074  
tttcagaaga aaggttggaa acaca 25

<210> 1075  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_102179\_29\_Forward\_Primer

<400> 1075  
aatctcgatt gtcttcttgc gaaat 25

<210> 1076  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_102179\_29\_Reverse\_Primer

<400> 1076  
tccaacaagt caacaatcaa gcaata 26

<210> 1077  
<211> 25  
<212> DNA  
<213> Glycine max



<223> Seq ID: 515002\_region\_G2\_\_2646\_15\_Forward\_Primer  
<400> 1077  
ccaaaggctt agtttcattt gcatt 25  
  
<210> 1078  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_2646\_15\_Reverse\_Primer  
<400> 1078  
gaaataaaca aatccaactt ctctcg 26  
  
<210> 1079  
<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_76652\_24\_Forward\_Primer  
<400> 1079  
actaactctt gcgtgctcct tgttt 25  
  
<210> 1080  
<211> 24  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_76652\_24\_Reverse\_Primer  
<400> 1080  
ccctgggaca tatactggat caaa 24  
  
<210> 1081  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_66280\_14\_Forward\_Primer  
<400> 1081  
gtgtagatt gattaaagtt cgctga 26  
  
<210> 1082  
<211> 26  
<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_66280\_14\_Reverse\_Primer

<400> 1082

agatttagcc catgattaaa gtgaaa 26

<210> 1083

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_54768\_13\_Forward\_Primer

<400> 1083

aaattaccaa tcatgtatgg agtgaga 27

<210> 1084

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_54768\_13\_Reverse\_Primer

<400> 1084

caggcacaat attgcaccat aactt 25

<210> 1085

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_62580\_14\_Forward\_Primer

<400> 1085

aacttatgga ccgttttgga gagat 25

<210> 1086

<211> 25

<212> DNA

<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_62580\_14\_Reverse\_Primer

<400> 1086

aaaggaggag caaagagtga agatt 25

<210> 1087

<211> 25  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_34598\_55\_Forward\_Primer  
  
<400> 1087  
  
aaagtctggt ctgaactgac ccatt 25  
  
<210> 1088  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_34598\_55\_Reverse\_Primer  
  
<400> 1088  
  
ggaatggaag ttatggagca gtaatgt 27  
  
<210> 1089  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_77680\_13\_Forward\_Primer  
  
<400> 1089  
  
tgacatgaac tatctcaaac aatgcaa 27  
  
<210> 1090  
<211> 26  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_77680\_13\_Reverse\_Primer  
  
<400> 1090  
  
aacaactgtt atttacacct cccaga 26  
  
<210> 1091  
<211> 27  
<212> DNA  
<213> Glycine max  
  
<223> Seq ID: 515002\_region\_G2\_\_77693\_12\_Forward\_Primer  
  
<400> 1091  
  
tgacatgaac tatctcaaac aatgcaa 27

<210> 1092  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_77693\_12\_Reverse\_Primer

<400> 1092

aacaactgtt atttacacct cccaga 26

<210> 1093  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_97392\_14\_Forward\_Primer

<400> 1093

tttgatgtag ttgatttatg cactcg 26

<210> 1094  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_97392\_14\_Reverse\_Primer

<400> 1094

gtgacatcag gcaacctagt ttagt 25

<210> 1095  
<211> 26  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_97359\_15\_Forward\_Primer

<400> 1095

tttgatgtag ttgatttatg cactcg 26

<210> 1096  
<211> 25  
<212> DNA  
<213> Glycine max

<223> Seq ID: 515002\_region\_G2\_\_97359\_15\_Reverse\_Primer

<400> 1096

gtgacatcag gcaacctagt ttagt

25

&lt;210&gt; 1097

&lt;211&gt; 877

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: 240017\_region\_G3

&lt;400&gt; 1097

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
 1 5 10 15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
 20 25 30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
 35 40 45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
 50 55 60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
 65 70 75 80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
 85 90 95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
 100 105 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
 115 120 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile  
 130 135 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
 145 150 155 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
 165 170 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
 180 185 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
 195 200 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
 210 215 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
 225 230 235 240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr

| 245 |     |     |     |     |     |     |     |     |     | 250 |     |     |     |     | 255 |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| His | Ser | Phe | Ser | Leu | Thr | Phe | Leu | Ser | Leu | Gln | Asn | Asn | Asn | Leu | Ser |  |  |  |  |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |  |  |  |  |
| Gly | Ser | Leu | Pro | Asn | Ser | Trp | Gly | Gly | Asn | Ser | Lys | Asn | Gly | Phe | Phe |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Arg | Leu | Gln | Asn | Leu | Ile | Leu | Asp | His | Asn | Phe | Phe | Thr | Gly | Asp | Val |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Pro | Ala | Ser | Leu | Gly | Ser | Leu | Arg | Glu | Leu | Asn | Glu | Ile | Ser | Leu | Ser |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |  |  |  |
| His | Asn | Lys | Phe | Ser | Gly | Ala | Ile | Pro | Asn | Glu | Ile | Gly | Thr | Leu | Ser |  |  |  |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |  |  |
| Arg | Leu | Lys | Thr | Leu | Asp | Ile | Ser | Asn | Asn | Ala | Leu | Asn | Gly | Asn | Leu |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |
| Pro | Ala | Thr | Leu | Ser | Asn | Leu | Ser | Ser | Leu | Thr | Leu | Leu | Asn | Ala | Glu |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |
| Asn | Asn | Leu | Leu | Asp | Asn | Gln | Ile | Pro | Gln | Ser | Leu | Gly | Arg | Leu | Arg |  |  |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Asn | Leu | Ser | Val | Leu | Ile | Leu | Ser | Arg | Asn | Gln | Phe | Ser | Gly | His | Ile |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |  |  |  |  |
| Pro | Ser | Ser | Ile | Ala | Asn | Ile | Ser | Ser | Leu | Arg | Gln | Leu | Asp | Leu | Ser |  |  |  |  |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |     |  |  |  |  |
| Leu | Asn | Asn | Phe | Ser | Gly | Glu | Ile | Pro | Val | Ser | Phe | Asp | Ser | Gln | Arg |  |  |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |  |
| Ser | Leu | Asn | Leu | Phe | Asn | Val | Ser | Tyr | Asn | Ser | Leu | Ser | Gly | Ser | Val |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |
| Pro | Pro | Leu | Leu | Ala | Lys | Lys | Phe | Asn | Ser | Ser | Ser | Phe | Val | Gly | Asn |  |  |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |
| Ile | Gln | Leu | Cys | Gly | Tyr | Ser | Pro | Ser | Thr | Pro | Cys | Leu | Ser | Gln | Ala |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |  |  |  |  |
| Pro | Ser | Gln | Gly | Val | Ile | Ala | Pro | Pro | Pro | Glu | Val | Ser | Lys | His | His |  |  |  |  |
|     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |     | 495 |     |  |  |  |  |
| His | His | Arg | Lys | Leu | Ser | Thr | Lys | Asp | Ile | Ile | Leu | Ile | Val | Ala | Gly |  |  |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |  |  |
| Val | Leu | Leu | Val | Val | Leu | Ile | Ile | Leu | Cys | Cys | Val | Leu | Leu | Phe | Cys |  |  |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |  |  |
| Leu | Ile | Arg | Lys | Arg | Ser | Thr | Ser | Lys | Ala | Gly | Asn | Gly | Gln | Ala | Thr |  |  |  |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |  |  |
| Glu | Gly | Arg | Ala | Ala | Thr | Met | Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val |  |  |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |     |  |  |  |  |

Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val  
 565 570 575  
 His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala  
 580 585 590  
 Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala  
 595 600 605  
 Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys  
 610 615 620  
 Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly  
 625 630 635 640  
 Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly  
 645 650 655  
 Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser  
 660 665 670  
 Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp  
 675 680 685  
 Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys  
 690 695 700  
 Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn  
 705 710 715 720  
 Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu  
 725 730 735  
 Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala  
 740 745 750  
 Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala  
 755 760 765  
 Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu  
 770 775 780  
 Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro  
 785 790 795 800  
 Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe  
 805 810 815  
 Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu  
 820 825 830  
 Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala  
 835 840 845  
 Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro  
 850 855 860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val  
 865 870 875

<210> 1098

<211> 854

<212> PRT

<213> Glycine max

<223> Seq ID: 240017\_region\_G3

<400> 1098

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  
 225 230 235 240



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Gln | Asn | Asn | Asn | Leu | Ser | Gly | Ser | Leu | Pro | Asn | Ser | Trp | 245 | 250 | 255 |     |
| Gly | Gly | Asn | Ser | Lys | Asn | Gly | Phe | Phe | Arg | Leu | Gln | Asn | Leu | Ile | Leu | 260 | 265 | 270 |     |
| Asp | His | Asn | Phe | Phe | Thr | Gly | Asp | Val | Pro | Ala | Ser | Leu | Gly | Ser | Leu | 275 | 280 | 285 |     |
| Arg | Glu | Leu | Asn | Glu | Ile | Ser | Leu | Ser | His | Asn | Lys | Phe | Ser | Gly | Ala | 290 | 295 | 300 |     |
| Ile | Pro | Asn | Glu | Ile | Gly | Thr | Leu | Ser | Arg | Leu | Lys | Thr | Leu | Asp | Ile | 305 | 310 | 315 | 320 |
| Ser | Asn | Asn | Ala | Leu | Asn | Gly | Asn | Leu | Pro | Ala | Thr | Leu | Ser | Asn | Leu | 325 | 330 | 335 |     |
| Ser | Ser | Leu | Thr | Leu | Leu | Asn | Ala | Glu | Asn | Asn | Leu | Leu | Asp | Asn | Gln | 340 | 345 | 350 |     |
| Ile | Pro | Gln | Ser | Leu | Gly | Arg | Leu | Arg | Asn | Leu | Ser | Val | Leu | Ile | Leu | 355 | 360 | 365 |     |
| Ser | Arg | Asn | Gln | Phe | Ser | Gly | His | Ile | Pro | Ser | Ser | Ile | Ala | Asn | Ile | 370 | 375 | 380 |     |
| Ser | Ser | Leu | Arg | Gln | Leu | Asp | Leu | Ser | Leu | Asn | Asn | Phe | Ser | Gly | Glu | 385 | 390 | 395 | 400 |
| Ile | Pro | Val | Ser | Phe | Asp | Ser | Gln | Arg | Ser | Leu | Asn | Leu | Phe | Asn | Val | 405 | 410 | 415 |     |
| Ser | Tyr | Asn | Ser | Leu | Ser | Gly | Ser | Val | Pro | Pro | Leu | Leu | Ala | Lys | Lys | 420 | 425 | 430 |     |
| Phe | Asn | Ser | Ser | Ser | Phe | Val | Gly | Asn | Ile | Gln | Leu | Cys | Gly | Tyr | Ser | 435 | 440 | 445 |     |
| Pro | Ser | Thr | Pro | Cys | Leu | Ser | Gln | Ala | Pro | Ser | Gln | Gly | Val | Ile | Ala | 450 | 455 | 460 |     |
| Pro | Pro | Pro | Glu | Val | Ser | Lys | His | His | His | His | Arg | Lys | Leu | Ser | Thr | 465 | 470 | 475 | 480 |
| Lys | Asp | Ile | Ile | Leu | Ile | Val | Ala | Gly | Val | Leu | Leu | Val | Val | Leu | Ile | 485 | 490 | 495 |     |
| Ile | Leu | Cys | Cys | Val | Leu | Leu | Phe | Cys | Leu | Ile | Arg | Lys | Arg | Ser | Thr | 500 | 505 | 510 |     |
| Ser | Lys | Ala | Gly | Asn | Gly | Gln | Ala | Thr | Glu | Gly | Arg | Ala | Ala | Thr | Met | 515 | 520 | 525 |     |
| Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val | Ala | Gly | Gly | Asp | Val | Glu | Ala | 530 | 535 | 540 |     |
| Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val | His | Phe | Asp | Gly | Pro | Met | Ala |     |     |     |     |

|                     |                         |                         |     |     |     |     |
|---------------------|-------------------------|-------------------------|-----|-----|-----|-----|
| 545                 |                         | 550                     |     | 555 |     | 560 |
| Phe Thr Ala Asp Asp | Leu Leu Cys Ala Thr     | Ala Glu Ile Met Gly Lys |     |     |     |     |
|                     | 565                     |                         | 570 |     | 575 |     |
| Ser Thr Tyr Gly Thr | Val Tyr Lys Ala Ile     | Leu Glu Asp Gly Ser Gln |     |     |     |     |
|                     | 580                     |                         | 585 |     | 590 |     |
| Val Ala Val Lys Arg | Leu Arg Glu Lys Ile Thr | Lys Gly His Arg Glu     |     |     |     |     |
|                     | 595                     |                         | 600 |     | 605 |     |
| Phe Glu Ser Glu Val | Ser Val Leu Gly Lys Ile | Arg His Pro Asn Val     |     |     |     |     |
|                     | 610                     |                         | 615 |     | 620 |     |
| Leu Ala Leu Arg Ala | Tyr Tyr Leu Gly Pro     | Lys Gly Glu Lys Leu Leu |     |     |     |     |
|                     | 625                     |                         | 630 |     | 635 |     |
| Val Phe Asp Tyr Met | Ser Lys Gly Ser Leu     | Ala Ser Phe Leu His Gly |     |     |     |     |
|                     | 645                     |                         | 650 |     | 655 |     |
| Gly Gly Thr Glu Thr | Phe Ile Asp Trp Pro     | Thr Arg Met Lys Ile Ala |     |     |     |     |
|                     | 660                     |                         | 665 |     | 670 |     |
| Gln Asp Leu Ala Arg | Gly Leu Phe Cys Leu     | His Ser Gln Glu Asn Ile |     |     |     |     |
|                     | 675                     |                         | 680 |     | 685 |     |
| Ile His Gly Asn Leu | Thr Ser Ser Asn Val     | Leu Leu Asp Glu Asn Thr |     |     |     |     |
|                     | 690                     |                         | 695 |     | 700 |     |
| Asn Ala Lys Ile Ala | Asp Phe Gly Leu Ser     | Arg Leu Met Ser Thr Ala |     |     |     |     |
|                     | 705                     |                         | 710 |     | 715 |     |
| Ala Asn Ser Asn Val | Ile Ala Thr Ala Gly     | Ala Leu Gly Tyr Arg Ala |     |     |     |     |
|                     | 725                     |                         | 730 |     | 735 |     |
| Pro Glu Leu Ser Lys | Leu Lys Lys Ala Asn     | Thr Lys Thr Asp Ile Tyr |     |     |     |     |
|                     | 740                     |                         | 745 |     | 750 |     |
| Ser Leu Gly Val Ile | Leu Leu Glu Leu Leu     | Thr Arg Lys Ser Pro Gly |     |     |     |     |
|                     | 755                     |                         | 760 |     | 765 |     |
| Val Ser Met Asn Gly | Leu Asp Leu Pro Gln     | Trp Val Ala Ser Val Val |     |     |     |     |
|                     | 770                     |                         | 775 |     | 780 |     |
| Lys Glu Glu Trp Thr | Asn Glu Val Phe Asp     | Ala Asp Leu Met Arg Asp |     |     |     |     |
|                     | 785                     |                         | 790 |     | 795 |     |
| Ala Ser Thr Val Gly | Asp Glu Leu Leu Asn     | Thr Leu Lys Leu Ala Leu |     |     |     |     |
|                     | 805                     |                         | 810 |     | 815 |     |
| His Cys Val Asp Pro | Ser Pro Ser Ala Arg     | Pro Glu Val His Gln Val |     |     |     |     |
|                     | 820                     |                         | 825 |     | 830 |     |
| Leu Gln Gln Leu Glu | Glu Ile Arg Pro Glu     | Arg Ser Val Thr Ala Ser |     |     |     |     |
|                     | 835                     |                         | 840 |     | 845 |     |
| Pro Gly Asp Asp Ile | Val                     |                         |     |     |     |     |
|                     | 850                     |                         |     |     |     |     |

<210> 1099  
 <211> 894  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: 318013\_region\_A3  
  
 <400> 1099  
  
 Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser  
 1 5 10 15  
  
 Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser  
 20 25 30  
  
 Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr  
 35 40 45  
  
 Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu  
 50 55 60  
  
 Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser  
 65 70 75 80  
  
 Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser  
 85 90 95  
  
 Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly  
 100 105 110  
  
 Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser  
 115 120 125  
  
 Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly  
 130 135 140  
  
 Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg  
 145 150 155 160  
  
 Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala  
 165 170 175  
  
 Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu  
 180 185 190  
  
 Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser  
 195 200 205  
  
 Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln  
 210 215 220  
  
 Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly  
 225 230 235 240  
  
 Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser  
 245 250 255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly  
 260 265 270  
 Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro  
 275 280 285  
 Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala  
 290 295 300  
 Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro  
 305 310 315 320  
 Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr  
 325 330 335  
 Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe  
 340 345 350  
 Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu  
 355 360 365  
 Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr  
 370 375 380  
 Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro  
 385 390 395 400  
 Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro  
 405 410 415  
 Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser  
 420 425 430  
 Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser  
 435 440 445  
 Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala  
 450 455 460  
 Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly  
 465 470 475 480  
 Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys  
 485 490 495  
 Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu  
 500 505 510  
 Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp  
 515 520 525  
 Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe  
 530 535 540  
 Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys  
 545 550 555 560

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Leu | His | Asp | Gly | Thr | Lys | Ile | Ala | Val | Lys | Arg | Met | Glu | Ser | 565 | 570 | 575 |     |
| Val | Ala | Met | Gly | Asn | Lys | Gly | Gln | Lys | Glu | Phe | Glu | Ala | Glu | Ile | Ala | 580 | 585 | 590 |     |
| Leu | Leu | Ser | Lys | Val | Arg | His | Arg | His | Leu | Val | Ala | Leu | Leu | Gly | Tyr | 595 | 600 | 605 |     |
| Cys | Ile | Asn | Gly | Asn | Glu | Arg | Leu | Leu | Val | Tyr | Glu | Tyr | Met | Pro | Gln | 610 | 615 | 620 |     |
| Gly | Thr | Leu | Thr | Gln | His | Leu | Phe | Glu | Trp | Gln | Glu | His | Gly | Tyr | Ala | 625 | 630 | 635 | 640 |
| Pro | Leu | Thr | Trp | Lys | Gln | Arg | Val | Val | Ile | Ala | Leu | Asp | Val | Ala | Arg | 645 | 650 | 655 |     |
| Gly | Val | Glu | Tyr | Leu | His | Ser | Leu | Ala | Gln | Gln | Ser | Phe | Ile | His | Arg | 660 | 665 | 670 |     |
| Asp | Leu | Lys | Pro | Ser | Asn | Ile | Leu | Leu | Gly | Asp | Asp | Met | Arg | Ala | Lys | 675 | 680 | 685 |     |
| Val | Ala | Asp | Phe | Gly | Leu | Val | Lys | Asn | Ala | Pro | Asp | Gly | Lys | Tyr | Ser | 690 | 695 | 700 |     |
| Val | Glu | Thr | Arg | Leu | Ala | Gly | Thr | Phe | Gly | Tyr | Leu | Ala | Pro | Glu | Tyr | 705 | 710 | 715 | 720 |
| Ala | Ala | Thr | Gly | Arg | Val | Thr | Thr | Lys | Val | Asp | Val | Tyr | Ala | Phe | Gly | 725 | 730 | 735 |     |
| Val | Val | Leu | Met | Glu | Leu | Ile | Thr | Gly | Arg | Lys | Ala | Leu | Asp | Asp | Thr | 740 | 745 | 750 |     |
| Val | Pro | Asp | Glu | Arg | Ser | His | Leu | Val | Thr | Trp | Phe | Arg | Arg | Val | Leu | 755 | 760 | 765 |     |
| Ile | Asn | Lys | Glu | Asn | Ile | Pro | Lys | Ala | Ile | Asp | Gln | Ile | Leu | Asn | Pro | 770 | 775 | 780 |     |
| Asp | Glu | Glu | Thr | Met | Gly | Ser | Ile | Tyr | Thr | Val | Ala | Glu | Leu | Ala | Gly | 785 | 790 | 795 | 800 |
| His | Cys | Thr | Ala | Arg | Glu | Pro | Tyr | Gln | Arg | Pro | Asp | Met | Gly | His | Ala | 805 | 810 | 815 |     |
| Val | Asn | Val | Leu | Val | Pro | Leu | Val | Glu | Gln | Trp | Lys | Pro | Thr | Ser | His | 820 | 825 | 830 |     |
| Asp | Glu | Glu | Glu | Glu | Asp | Gly | Ser | Gly | Gly | Asp | Leu | His | Met | Ser | Leu | 835 | 840 | 845 |     |
| Pro | Gln | Ala | Leu | Arg | Arg | Trp | Gln | Ala | Asn | Glu | Gly | Thr | Ser | Ser | Ile | 850 | 855 | 860 |     |
| Phe | Asn | Asp | Ile | Ser | Ile | Ser | Gln | Thr | Gln | Ser | Ser | Ile | Ser | Ser | Lys |     |     |     |     |

|   |                             |                     |     |
|---|-----------------------------|---------------------|-----|
| 865   | 870                         | 875                 | 880 |
| Pro Ala Gly Phe   | Ala Asp Ser Phe Asp         | Ser Met Asp Cys Arg |     |
|   | 885                         | 890                 |     |
| <210>   | 1100                        |                     |     |
| <211>   | 877                         |                     |     |
| <212>   | PRT                         |                     |     |
| <213>   | Glycine max                 |                     |     |
| <223>   | Seq ID: rhg1_A3244_amplicon |                     |     |
| <400>   | 1100                        |                     |     |
| Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp |                             |                     |     |
| 1   | 5                           | 10                  | 15  |
| Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg |                             |                     |     |
|   | 20                          | 25                  | 30  |
| Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr |                             |                     |     |
|   | 35                          | 40                  | 45  |
| Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val |                             |                     |     |
| 50  | 55                          | 60                  |     |
| Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg |                             |                     |     |
| 65  | 70                          | 75                  | 80  |
| Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala |                             |                     |     |
|   | 85                          | 90                  | 95  |
| Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro |                             |                     |     |
|   | 100                         | 105                 | 110 |
| Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser |                             |                     |     |
|   | 115                         | 120                 | 125 |
| Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile |                             |                     |     |
| 130   | 135                         | 140                 |     |
| Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly |                             |                     |     |
| 145   | 150                         | 155                 | 160 |
| Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly |                             |                     |     |
|   | 165                         | 170                 | 175 |
| Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val |                             |                     |     |
|   | 180                         | 185                 | 190 |
| Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly |                             |                     |     |
|   | 195                         | 200                 | 205 |
| Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr |                             |                     |     |
| 210   | 215                         | 220                 |     |
| Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu |                             |                     |     |

|                 |                     |                     |             |     |  |     |
|-----------------|---------------------|---------------------|-------------|-----|--|-----|
| 225             |                     | 230                 |             | 235 |  | 240 |
| Asn Leu Ser Phe | Asn Ser Phe Ser Gly | Pro Leu Pro Ala Ser | Leu Thr     |     |  |     |
|                 | 245                 | 250                 | 255         |     |  |     |
| His Ser Phe Ser | Leu Thr Phe Leu Ser | Leu Gln Asn Asn Asn | Leu Ser     |     |  |     |
|                 | 260                 | 265                 | 270         |     |  |     |
| Gly Ser Leu Pro | Asn Ser Trp Gly Gly | Asn Ser Lys Asn Gly | Phe Phe     |     |  |     |
|                 | 275                 | 280                 | 285         |     |  |     |
| Arg Leu Gln Asn | Leu Ile Leu Asp His | Asn Phe Phe Thr     | Gly Asp Val |     |  |     |
|                 | 290                 | 295                 | 300         |     |  |     |
| Pro Ala Ser Leu | Gly Ser Leu Arg Glu | Leu Asn Glu Ile Ser | Leu Ser     |     |  |     |
|                 | 305                 | 310                 | 315         | 320 |  |     |
| His Asn Lys Phe | Ser Gly Ala Ile Pro | Asn Glu Ile Gly Thr | Leu Ser     |     |  |     |
|                 | 325                 | 330                 | 335         |     |  |     |
| Arg Leu Lys Thr | Leu Asp Ile Ser Asn | Asn Ala Leu Asn Gly | Asn Leu     |     |  |     |
|                 | 340                 | 345                 | 350         |     |  |     |
| Pro Ala Thr Leu | Ser Asn Leu Ser Ser | Leu Thr Leu Leu     | Asn Ala Glu |     |  |     |
|                 | 355                 | 360                 | 365         |     |  |     |
| Asn Asn Leu Leu | Asp Asn Gln Ile Pro | Gln Ser Leu Gly Arg | Leu Arg     |     |  |     |
|                 | 370                 | 375                 | 380         |     |  |     |
| Asn Leu Ser Val | Leu Ile Leu Ser Arg | Asn Gln Phe Ser Gly | His Ile     |     |  |     |
|                 | 385                 | 390                 | 395         | 400 |  |     |
| Pro Ser Ser Ile | Ala Asn Ile Ser Ser | Leu Arg Gln Leu Asp | Leu Ser     |     |  |     |
|                 | 405                 | 410                 | 415         |     |  |     |
| Leu Asn Asn Phe | Ser Gly Glu Ile Pro | Val Ser Phe Asp Ser | Gln Arg     |     |  |     |
|                 | 420                 | 425                 | 430         |     |  |     |
| Ser Leu Asn Leu | Phe Asn Val Ser Tyr | Asn Ser Leu Ser Gly | Ser Val     |     |  |     |
|                 | 435                 | 440                 | 445         |     |  |     |
| Pro Pro Leu Leu | Ala Lys Lys Phe Asn | Ser Ser Ser Phe Val | Gly Asn     |     |  |     |
|                 | 450                 | 455                 | 460         |     |  |     |
| Ile Gln Leu Cys | Gly Tyr Ser Pro Ser | Thr Pro Cys Leu Ser | Gln Ala     |     |  |     |
|                 | 465                 | 470                 | 475         | 480 |  |     |
| Pro Ser Gln Gly | Val Ile Ala Pro Pro | Pro Glu Val Ser Lys | His His     |     |  |     |
|                 | 485                 | 490                 | 495         |     |  |     |
| His His Arg Lys | Leu Ser Thr Lys Asp | Ile Ile Leu Ile Val | Ala Gly     |     |  |     |
|                 | 500                 | 505                 | 510         |     |  |     |
| Val Leu Leu Val | Val Leu Ile Ile Leu | Cys Cys Val Leu Leu | Phe Cys     |     |  |     |
|                 | 515                 | 520                 | 525         |     |  |     |
| Leu Ile Arg Lys | Arg Ser Thr Ser Lys | Ala Gly Asn Gly Gln | Ala Thr     |     |  |     |
|                 | 530                 | 535                 | 540         |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Arg | Ala | Ala | Thr | Met | Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val |
| 545 |     |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     | 560 |
| Ala | Gly | Gly | Asp | Val | Glu | Ala | Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| His | Phe | Asp | Gly | Pro | Met | Ala | Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Thr | Ala | Glu | Ile | Met | Gly | Lys | Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ile | Leu | Glu | Asp | Gly | Ser | Gln | Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ile | Thr | Lys | Gly | His | Arg | Glu | Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     | 640 |     |
| Lys | Ile | Arg | His | Pro | Asn | Val | Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Pro | Lys | Gly | Glu | Lys | Leu | Leu | Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser |
|     |     |     | 660 |     |     |     |     |     | 665 |     |     |     | 670 |     |     |
| Leu | Ala | Ser | Phe | Leu | His | Gly | Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Pro | Thr | Arg | Met | Lys | Ile | Ala | Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Leu | His | Ser | Gln | Glu | Asn | Ile | Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Val | Leu | Leu | Asp | Glu | Asn | Thr | Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     | 735 |     |     |
| Ser | Arg | Leu | Met | Ser | Thr | Ala | Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     | 750 |     |     |     |
| Gly | Ala | Leu | Gly | Tyr | Arg | Ala | Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Asn | Thr | Lys | Thr | Asp | Ile | Tyr | Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Leu | Thr | Arg | Lys | Ser | Pro | Gly | Val | Ser | Met | Asn | Gly | Leu | Asp | Leu | Pro |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     | 800 |     |
| Gln | Trp | Val | Ala | Ser | Val | Val | Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     | 815 |     |     |
| Asp | Ala | Asp | Leu | Met | Arg | Asp | Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     | 830 |     |     |     |
| Asn | Thr | Leu | Lys | Leu | Ala | Leu | His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |



```

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro
      850                855                860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val
865                870                875

<210>      1101
<211>      854
<212>      PRT
<213>      Glycine max

<223>      Seq ID: rhg1_A3244_amplicon

<400>      1101

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys
1                5                10                15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met
      20                25                30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser
      35                40                45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu
      50                55                60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu
65                70                75                80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp
      85                90                95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys
      100                105                110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu
      115                120                125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys
      130                135                140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu
145                150                155                160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu
      165                170                175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser
      180                185                190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu
      195                200                205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe
      210                215                220

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Pro | Leu | Pro | Ala | Ser | Leu | Thr | His | Ser | Phe | Ser | Leu | Thr | Phe | 225 |     | 230 |     | 235 |     | 240 |
| Leu | Ser | Leu | Gln | Asn | Asn | Asn | Leu | Ser | Gly | Ser | Leu | Pro | Asn | Ser | Trp |     | 245 |     | 250 |     | 255 |     |
| Gly | Gly | Asn | Ser | Lys | Asn | Gly | Phe | Phe | Arg | Leu | Gln | Asn | Leu | Ile | Leu |     | 260 |     | 265 |     | 270 |     |
| Asp | His | Asn | Phe | Phe | Thr | Gly | Asp | Val | Pro | Ala | Ser | Leu | Gly | Ser | Leu | 275 |     | 280 |     | 285 |     |     |
| Arg | Glu | Leu | Asn | Glu | Ile | Ser | Leu | Ser | His | Asn | Lys | Phe | Ser | Gly | Ala | 290 |     | 295 |     | 300 |     |     |
| Ile | Pro | Asn | Glu | Ile | Gly | Thr | Leu | Ser | Arg | Leu | Lys | Thr | Leu | Asp | Ile | 305 |     | 310 |     | 315 |     | 320 |
| Ser | Asn | Asn | Ala | Leu | Asn | Gly | Asn | Leu | Pro | Ala | Thr | Leu | Ser | Asn | Leu |     | 325 |     | 330 |     | 335 |     |
| Ser | Ser | Leu | Thr | Leu | Leu | Asn | Ala | Glu | Asn | Asn | Leu | Leu | Asp | Asn | Gln |     | 340 |     | 345 |     | 350 |     |
| Ile | Pro | Gln | Ser | Leu | Gly | Arg | Leu | Arg | Asn | Leu | Ser | Val | Leu | Ile | Leu |     | 355 |     | 360 |     | 365 |     |
| Ser | Arg | Asn | Gln | Phe | Ser | Gly | His | Ile | Pro | Ser | Ser | Ile | Ala | Asn | Ile | 370 |     | 375 |     | 380 |     |     |
| Ser | Ser | Leu | Arg | Gln | Leu | Asp | Leu | Ser | Leu | Asn | Asn | Phe | Ser | Gly | Glu | 385 |     | 390 |     | 395 |     | 400 |
| Ile | Pro | Val | Ser | Phe | Asp | Ser | Gln | Arg | Ser | Leu | Asn | Leu | Phe | Asn | Val |     | 405 |     | 410 |     | 415 |     |
| Ser | Tyr | Asn | Ser | Leu | Ser | Gly | Ser | Val | Pro | Pro | Leu | Leu | Ala | Lys | Lys |     | 420 |     | 425 |     | 430 |     |
| Phe | Asn | Ser | Ser | Ser | Phe | Val | Gly | Asn | Ile | Gln | Leu | Cys | Gly | Tyr | Ser |     | 435 |     | 440 |     | 445 |     |
| Pro | Ser | Thr | Pro | Cys | Leu | Ser | Gln | Ala | Pro | Ser | Gln | Gly | Val | Ile | Ala | 450 |     | 455 |     | 460 |     |     |
| Pro | Pro | Pro | Glu | Val | Ser | Lys | His | His | His | His | Arg | Lys | Leu | Ser | Thr | 465 |     | 470 |     | 475 |     | 480 |
| Lys | Asp | Ile | Ile | Leu | Ile | Val | Ala | Gly | Val | Leu | Leu | Val | Val | Leu | Ile |     | 485 |     | 490 |     | 495 |     |
| Ile | Leu | Cys | Cys | Val | Leu | Leu | Phe | Cys | Leu | Ile | Arg | Lys | Arg | Ser | Thr |     | 500 |     | 505 |     | 510 |     |
| Ser | Lys | Ala | Gly | Asn | Gly | Gln | Ala | Thr | Glu | Gly | Arg | Ala | Ala | Thr | Met |     | 515 |     | 520 |     | 525 |     |
| Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val | Ala | Gly | Gly | Asp | Val | Glu | Ala |     |     |     |     |     |     |     |

|   |  |     |  |     |     |
|---|--|-----|--|-----|-----|
| 530   |  | 535 |  | 540 |     |
| Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala |  |     |  |     |     |
| 545   |  | 550 |  | 555 | 560 |
| Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys |  |     |  |     |     |
|   |  | 565 |  | 570 | 575 |
| Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln |  |     |  |     |     |
|   |  | 580 |  | 585 | 590 |
| Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu |  |     |  |     |     |
|   |  | 595 |  | 600 | 605 |
| Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val |  |     |  |     |     |
|   |  | 610 |  | 615 | 620 |
| Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu |  |     |  |     |     |
|   |  | 625 |  | 630 | 635 |
| Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly |  |     |  |     |     |
|   |  | 645 |  | 650 | 655 |
| Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala |  |     |  |     |     |
|   |  | 660 |  | 665 | 670 |
| Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile |  |     |  |     |     |
|   |  | 675 |  | 680 | 685 |
| Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr |  |     |  |     |     |
|   |  | 690 |  | 695 | 700 |
| Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala |  |     |  |     |     |
|   |  | 705 |  | 710 | 715 |
| Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala |  |     |  |     |     |
|   |  | 725 |  | 730 | 735 |
| Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr |  |     |  |     |     |
|   |  | 740 |  | 745 | 750 |
| Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly |  |     |  |     |     |
|   |  | 755 |  | 760 | 765 |
| Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val |  |     |  |     |     |
|   |  | 770 |  | 775 | 780 |
| Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp |  |     |  |     |     |
|   |  | 785 |  | 790 | 795 |
| Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu |  |     |  |     |     |
|   |  | 805 |  | 810 | 815 |
| His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val |  |     |  |     |     |
|   |  | 820 |  | 825 | 830 |
| Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser |  |     |  |     |     |
|   |  | 835 |  | 840 | 845 |

Pro Gly Asp Asp Ile Val  
850

<210> 1102

<211> 877

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_peking\_amplicon

<400> 1102

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
1 5 10 15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
20 25 30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
35 40 45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
50 55 60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
65 70 75 80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
85 90 95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Ala Asp Pro  
100 105 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
115 120 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile  
130 135 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
145 150 155 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
165 170 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
180 185 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
195 200 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
210 215 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
225 230 235 240

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Ser | Phe | Asn | Ser | Phe | Ser | Gly | Pro | Leu | Pro | Ala | Ser | Leu | Thr | 245 | 250 | 255 |
| His | Ser | Phe | Ser | Leu | Thr | Phe | Leu | Ser | Leu | Gln | Asn | Asn | Asn | Leu | Ser | 260 | 265 | 270 |
| Gly | Ser | Leu | Pro | Asn | Ser | Trp | Gly | Gly | Asn | Ser | Lys | Asn | Gly | Phe | Phe | 275 | 280 | 285 |
| Arg | Leu | Gln | Asn | Leu | Ile | Leu | Asp | His | Asn | Phe | Phe | Thr | Gly | Asp | Val | 290 | 295 | 300 |
| Pro | Ala | Ser | Leu | Gly | Ser | Leu | Arg | Glu | Leu | Asn | Glu | Ile | Ser | Leu | Ser | 305 | 310 | 315 |
| His | Asn | Lys | Phe | Ser | Gly | Ala | Ile | Pro | Asn | Glu | Ile | Gly | Thr | Leu | Ser | 325 | 330 | 335 |
| Arg | Leu | Lys | Thr | Leu | Asp | Ile | Ser | Asn | Asn | Ala | Leu | Asn | Gly | Asn | Leu | 340 | 345 | 350 |
| Pro | Ala | Thr | Leu | Ser | Asn | Leu | Ser | Ser | Leu | Thr | Leu | Leu | Asn | Ala | Glu | 355 | 360 | 365 |
| Asn | Asn | Leu | Leu | Asp | Asn | Gln | Ile | Pro | Gln | Ser | Leu | Gly | Arg | Leu | Arg | 370 | 375 | 380 |
| Asn | Leu | Ser | Val | Leu | Ile | Leu | Ser | Arg | Asn | Gln | Phe | Ser | Gly | His | Ile | 385 | 390 | 395 |
| Pro | Ser | Ser | Ile | Ala | Asn | Ile | Ser | Ser | Leu | Arg | Gln | Leu | Asp | Leu | Ser | 405 | 410 | 415 |
| Leu | Asn | Asn | Phe | Ser | Gly | Glu | Ile | Pro | Val | Ser | Phe | Asp | Ser | Gln | Arg | 420 | 425 | 430 |
| Ser | Leu | Asn | Leu | Phe | Asn | Val | Ser | Tyr | Asn | Ser | Leu | Ser | Gly | Ser | Val | 435 | 440 | 445 |
| Pro | Pro | Leu | Leu | Ala | Lys | Lys | Phe | Asn | Ser | Ser | Ser | Phe | Val | Gly | Asn | 450 | 455 | 460 |
| Ile | Gln | Leu | Cys | Gly | Tyr | Ser | Pro | Ser | Thr | Pro | Cys | Leu | Ser | Gln | Ala | 465 | 470 | 475 |
| Pro | Ser | Gln | Gly | Val | Ile | Ala | Pro | Pro | Pro | Glu | Val | Ser | Lys | His | His | 485 | 490 | 495 |
| His | His | Arg | Lys | Leu | Ser | Thr | Lys | Asp | Ile | Ile | Leu | Ile | Val | Ala | Gly | 500 | 505 | 510 |
| Val | Leu | Leu | Val | Val | Leu | Ile | Ile | Leu | Cys | Cys | Val | Leu | Leu | Phe | Cys | 515 | 520 | 525 |
| Leu | Ile | Arg | Lys | Arg | Ser | Thr | Ser | Lys | Ala | Gly | Asn | Gly | Gln | Ala | Thr | 530 | 535 | 540 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Arg | Ala | Ala | Thr | Met | Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val | 545 | 550 | 555 | 560 |
| Ala | Gly | Gly | Asp | Val | Glu | Ala | Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val | 565 | 570 | 575 |     |
| His | Phe | Asp | Gly | Pro | Met | Ala | Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala | 580 | 585 | 590 |     |
| Thr | Ala | Glu | Ile | Met | Gly | Lys | Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala | 595 | 600 | 605 |     |
| Ile | Leu | Glu | Asp | Gly | Ser | Gln | Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys | 610 | 615 | 620 |     |
| Ile | Thr | Lys | Gly | His | Arg | Glu | Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly | 625 | 630 | 635 | 640 |
| Lys | Ile | Arg | His | Pro | Asn | Val | Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly | 645 | 650 | 655 |     |
| Pro | Lys | Gly | Glu | Lys | Leu | Leu | Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser | 660 | 665 | 670 |     |
| Leu | Ala | Ser | Phe | Leu | His | Gly | Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp | 675 | 680 | 685 |     |
| Pro | Thr | Arg | Met | Lys | Ile | Ala | Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys | 690 | 695 | 700 |     |
| Leu | His | Ser | Gln | Glu | Asn | Ile | Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn | 705 | 710 | 715 | 720 |
| Val | Leu | Leu | Asp | Glu | Asn | Thr | Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu | 725 | 730 | 735 |     |
| Ser | Arg | Leu | Met | Ser | Thr | Ala | Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala | 740 | 745 | 750 |     |
| Gly | Ala | Leu | Gly | Tyr | Arg | Ala | Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala | 755 | 760 | 765 |     |
| Asn | Thr | Lys | Thr | Asp | Ile | Tyr | Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu | 770 | 775 | 780 |     |
| Leu | Thr | Arg | Lys | Ser | Pro | Gly | Val | Ser | Met | Asn | Gly | Leu | Asp | Leu | Pro | 785 | 790 | 795 | 800 |
| Gln | Trp | Val | Ala | Ser | Val | Val | Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe | 805 | 810 | 815 |     |
| Asp | Ala | Asp | Leu | Met | Arg | Asp | Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu | 820 | 825 | 830 |     |
| Asn | Thr | Leu | Lys | Leu | Ala | Leu | His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala | 835 | 840 | 845 |     |
| Arg | Pro | Glu | Val | His | Gln | Val | Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro |     |     |     |     |

|  |     |         |
|--|-----|---------|
| 850  | 855 | 860     |
| Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val  |     |         |
| 865  | 870 | 875     |
| <p>&lt;210&gt; 1103</p> <p>&lt;211&gt; 854</p> <p>&lt;212&gt; PRT</p> <p>&lt;213&gt; Glycine max</p> <p>&lt;223&gt; Seq ID: rhg1_peking_amplicon</p> <p>&lt;400&gt; 1103</p> |     |         |
| Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  |     |         |
| 1  | 5   | 10 15   |
| Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  |     |         |
|  | 20  | 25 30   |
| Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  |     |         |
|  | 35  | 40 45   |
| Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  |     |         |
|  | 50  | 55 60   |
| Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  |     |         |
| 65   | 70  | 75 80   |
| Ala Phe Lys Gln Glu Leu Ala Asp Pro Glu Gly Phe Leu Arg Ser Trp  |     |         |
|  | 85  | 90 95   |
| Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  |     |         |
|  | 100 | 105 110 |
| Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  |     |         |
|  | 115 | 120 125 |
| Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  |     |         |
|  | 130 | 135 140 |
| Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  |     |         |
| 145  | 150 | 155 160 |
| Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  |     |         |
|  | 165 | 170 175 |
| Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  |     |         |
|  | 180 | 185 190 |
| Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  |     |         |
|  | 195 | 200 205 |
| Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  |     |         |
| 210  | 215 | 220     |
| Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  |     |         |

|   |  |     |  |     |  |     |
|---|--|-----|--|-----|--|-----|
| 225   |  | 230 |  | 235 |  | 240 |
| Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp |  |     |  |     |  |     |
|   |  | 245 |  | 250 |  | 255 |
| Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu |  |     |  |     |  |     |
|   |  | 260 |  | 265 |  | 270 |
| Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu |  |     |  |     |  |     |
|   |  | 275 |  | 280 |  | 285 |
| Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala |  |     |  |     |  |     |
|   |  | 290 |  | 295 |  | 300 |
| Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile |  |     |  |     |  |     |
|   |  | 305 |  | 310 |  | 315 |
| Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu |  |     |  |     |  |     |
|   |  | 325 |  | 330 |  | 335 |
| Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln |  |     |  |     |  |     |
|   |  | 340 |  | 345 |  | 350 |
| Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu |  |     |  |     |  |     |
|   |  | 355 |  | 360 |  | 365 |
| Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile |  |     |  |     |  |     |
|   |  | 370 |  | 375 |  | 380 |
| Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu |  |     |  |     |  |     |
|   |  | 385 |  | 390 |  | 395 |
| Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val |  |     |  |     |  |     |
|   |  | 405 |  | 410 |  | 415 |
| Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys |  |     |  |     |  |     |
|   |  | 420 |  | 425 |  | 430 |
| Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser |  |     |  |     |  |     |
|   |  | 435 |  | 440 |  | 445 |
| Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala |  |     |  |     |  |     |
|   |  | 450 |  | 455 |  | 460 |
| Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr |  |     |  |     |  |     |
|   |  | 465 |  | 470 |  | 475 |
| Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile |  |     |  |     |  |     |
|   |  | 485 |  | 490 |  | 495 |
| Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr |  |     |  |     |  |     |
|   |  | 500 |  | 505 |  | 510 |
| Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met |  |     |  |     |  |     |
|   |  | 515 |  | 520 |  | 525 |
| Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala |  |     |  |     |  |     |
|   |  | 530 |  | 535 |  | 540 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val | His | Phe | Asp | Gly | Pro | Met | Ala |  |
| 545 |     |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     | 560 |  |
| Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala | Thr | Ala | Glu | Ile | Met | Gly | Lys |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |
| Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala | Ile | Leu | Glu | Asp | Gly | Ser | Gln |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |
| Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys | Ile | Thr | Lys | Gly | His | Arg | Glu |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |
| Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly | Lys | Ile | Arg | His | Pro | Asn | Val |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |
| Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly | Pro | Lys | Gly | Glu | Lys | Leu | Leu |  |
| 625 |     |     |     |     |     | 630 |     |     |     | 635 |     |     |     |     | 640 |  |
| Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser | Leu | Ala | Ser | Phe | Leu | His | Gly |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |
| Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp | Pro | Thr | Arg | Met | Lys | Ile | Ala |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |  |
| Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys | Leu | His | Ser | Gln | Glu | Asn | Ile |  |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |
| Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn | Val | Leu | Leu | Asp | Glu | Asn | Thr |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |
| Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu | Ser | Arg | Leu | Met | Ser | Thr | Ala |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |
| Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala | Gly | Ala | Leu | Gly | Tyr | Arg | Ala |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |
| Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala | Asn | Thr | Lys | Thr | Asp | Ile | Tyr |  |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |
| Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu | Leu | Thr | Arg | Lys | Ser | Pro | Gly |  |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |
| Val | Ser | Met | Asn | Gly | Leu | Asp | Leu | Pro | Gln | Trp | Val | Ala | Ser | Val | Val |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |
| Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe | Asp | Ala | Asp | Leu | Met | Arg | Asp |  |
| 785 |     |     |     |     | 790 |     |     |     | 795 |     |     |     |     |     | 800 |  |
| Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu | Asn | Thr | Leu | Lys | Leu | Ala | Leu |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |
| His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala | Arg | Pro | Glu | Val | His | Gln | Val |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |  |
| Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro | Glu | Arg | Ser | Val | Thr | Ala | Ser |  |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |  |

Pro Gly Asp Asp Ile Val  
850

<210> 1104

<211> 877

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_toyosuzu\_amplicon

<400> 1104

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
1 5 10 15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
20 25 30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
35 40 45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
50 55 60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
65 70 75 80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
85 90 95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
100 105 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
115 120 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile  
130 135 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
145 150 155 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
165 170 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
180 185 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
195 200 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
210 215 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
225 230 235 240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr  
 245 250 255  
 His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser  
 260 265 270  
 Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe  
 275 280 285  
 Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val  
 290 295 300  
 Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser  
 305 310 315 320  
 His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser  
 325 330 335  
 Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu  
 340 345 350  
 Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu  
 355 360 365  
 Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg  
 370 375 380  
 Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile  
 385 390 395 400  
 Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser  
 405 410 415  
 Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg  
 420 425 430  
 Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val  
 435 440 445  
 Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn  
 450 455 460  
 Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala  
 465 470 475 480  
 Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His  
 485 490 495  
 His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly  
 500 505 510  
 Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys  
 515 520 525  
 Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr  
 530 535 540  
 Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 545 |     |     |     |     | 550 |     |     |     |     |     | 555 |     |     |     | 560 |
| Ala | Gly | Gly | Asp | Val | Glu | Ala | Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| His | Phe | Asp | Gly | Pro | Met | Ala | Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Thr | Ala | Glu | Ile | Met | Gly | Lys | Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ile | Leu | Glu | Asp | Gly | Ser | Gln | Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ile | Thr | Lys | Gly | His | Arg | Glu | Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     | 640 |     |
| Lys | Ile | Arg | His | Pro | Asn | Val | Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly |
|     |     |     | 645 |     |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Pro | Lys | Gly | Glu | Lys | Leu | Leu | Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Leu | Ala | Ser | Phe | Leu | His | Gly | Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp |
|     |     | 675 |     |     |     | 680 |     |     |     |     |     | 685 |     |     |     |
| Pro | Thr | Arg | Met | Lys | Ile | Ala | Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Leu | His | Ser | Gln | Glu | Asn | Ile | Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Val | Leu | Leu | Asp | Glu | Asn | Thr | Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     | 735 |     |     |
| Ser | Arg | Leu | Met | Ser | Thr | Ala | Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Gly | Ala | Leu | Gly | Tyr | Arg | Ala | Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala |
|     |     | 755 |     |     |     | 760 |     |     |     |     |     | 765 |     |     |     |
| Asn | Thr | Lys | Thr | Asp | Ile | Tyr | Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu |
|     | 770 |     |     |     | 775 |     |     |     |     |     | 780 |     |     |     |     |
| Leu | Thr | Arg | Lys | Ser | Pro | Gly | Val | Ser | Met | Asn | Gly | Leu | Asp | Leu | Pro |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     | 800 |     |
| Gln | Trp | Val | Ala | Ser | Val | Val | Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe |
|     |     |     | 805 |     |     |     |     |     | 810 |     |     |     | 815 |     |     |
| Asp | Ala | Asp | Leu | Met | Arg | Asp | Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Asn | Thr | Leu | Lys | Leu | Ala | Leu | His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |
| Arg | Pro | Glu | Val | His | Gln | Val | Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val  
 865 870 875

<210> 1105

<211> 854

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_toyosuzu\_amplicon

<400> 1105

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110

Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe

|   |  |     |  |     |  |     |
|---|--|-----|--|-----|--|-----|
| 225   |  | 230 |  | 235 |  | 240 |
| Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp |  |     |  |     |  |     |
|   |  | 245 |  | 250 |  | 255 |
| Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu |  |     |  |     |  |     |
|   |  | 260 |  | 265 |  | 270 |
| Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu |  |     |  |     |  |     |
|   |  | 275 |  | 280 |  | 285 |
| Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala |  |     |  |     |  |     |
|   |  | 290 |  | 295 |  | 300 |
| Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile |  |     |  |     |  |     |
| 305   |  | 310 |  | 315 |  | 320 |
| Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu |  |     |  |     |  |     |
|   |  | 325 |  | 330 |  | 335 |
| Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln |  |     |  |     |  |     |
|   |  | 340 |  | 345 |  | 350 |
| Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu |  |     |  |     |  |     |
|   |  | 355 |  | 360 |  | 365 |
| Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile |  |     |  |     |  |     |
|   |  | 370 |  | 375 |  | 380 |
| Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu |  |     |  |     |  |     |
| 385   |  | 390 |  | 395 |  | 400 |
| Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val |  |     |  |     |  |     |
|   |  | 405 |  | 410 |  | 415 |
| Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys |  |     |  |     |  |     |
|   |  | 420 |  | 425 |  | 430 |
| Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser |  |     |  |     |  |     |
|   |  | 435 |  | 440 |  | 445 |
| Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala |  |     |  |     |  |     |
|   |  | 450 |  | 455 |  | 460 |
| Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr |  |     |  |     |  |     |
| 465   |  | 470 |  | 475 |  | 480 |
| Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile |  |     |  |     |  |     |
|   |  | 485 |  | 490 |  | 495 |
| Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr |  |     |  |     |  |     |
|   |  | 500 |  | 505 |  | 510 |
| Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met |  |     |  |     |  |     |
|   |  | 515 |  | 520 |  | 525 |
| Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala |  |     |  |     |  |     |
|   |  | 530 |  | 535 |  | 540 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Gly | Glu | Ala | Gly | Gly | Lys | Leu | Val | His | Phe | Asp | Gly | Pro | Met | Ala |  |
| 545 |     |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     | 560 |  |
| Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala | Thr | Ala | Glu | Ile | Met | Gly | Lys |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |
| Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala | Ile | Leu | Glu | Asp | Gly | Ser | Gln |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |
| Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys | Ile | Thr | Lys | Gly | His | Arg | Glu |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |
| Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly | Lys | Ile | Arg | His | Pro | Asn | Val |  |
| 610 |     |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |
| Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly | Pro | Lys | Gly | Glu | Lys | Leu | Leu |  |
| 625 |     |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     | 640 |  |
| Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser | Leu | Ala | Ser | Phe | Leu | His | Gly |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |
| Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp | Pro | Thr | Arg | Met | Lys | Ile | Ala |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |  |
| Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys | Leu | His | Ser | Gln | Glu | Asn | Ile |  |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |
| Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn | Val | Leu | Leu | Asp | Glu | Asn | Thr |  |
| 690 |     |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |
| Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu | Ser | Arg | Leu | Met | Ser | Thr | Ala |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |
| Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala | Gly | Ala | Leu | Gly | Tyr | Arg | Ala |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |
| Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala | Asn | Thr | Lys | Thr | Asp | Ile | Tyr |  |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |
| Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu | Leu | Thr | Arg | Lys | Ser | Pro | Gly |  |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |
| Val | Ser | Met | Asn | Gly | Leu | Asp | Leu | Pro | Gln | Trp | Val | Ala | Ser | Val | Val |  |
|     |     | 770 |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |
| Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe | Asp | Ala | Asp | Leu | Met | Arg | Asp |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |  |
| Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu | Asn | Thr | Leu | Lys | Leu | Ala | Leu |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |
| His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala | Arg | Pro | Glu | Val | His | Gln | Val |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |  |
| Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro | Glu | Arg | Ser | Val | Thr | Ala | Ser |  |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     |     | 845 |     |     |  |

Pro Gly Asp Asp Ile Val  
850

<210> 1106

<211> 877

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_will\_amplicon

<400> 1106

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
1 5 10 15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
20 25 30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
35 40 45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
50 55 60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
65 70 75 80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
85 90 95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
100 105 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
115 120 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile  
130 135 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
145 150 155 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
165 170 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
180 185 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
195 200 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
210 215 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
225 230 235 240



Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr  
 245 250 255  
 His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser  
 260 265 270  
 Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe  
 275 280 285  
 Arg Leu Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val  
 290 295 300  
 Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser  
 305 310 315 320  
 His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser  
 325 330 335  
 Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu  
 340 345 350  
 Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu  
 355 360 365  
 Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg  
 370 375 380  
 Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile  
 385 390 395 400  
 Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser  
 405 410 415  
 Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg  
 420 425 430  
 Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val  
 435 440 445  
 Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn  
 450 455 460  
 Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala  
 465 470 475 480  
 Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His  
 485 490 495  
 His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly  
 500 505 510  
 Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys  
 515 520 525  
 Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr  
 530 535 540  
 Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val

|   |     |     |  |     |  |     |
|---|-----|-----|--|-----|--|-----|
| 545   |     | 550 |  | 555 |  | 560 |
| Ala Gly Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val |     |     |  |     |  |     |
|   | 565 |     |  | 570 |  | 575 |
| His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala |     |     |  |     |  |     |
|   | 580 |     |  | 585 |  | 590 |
| Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala |     |     |  |     |  |     |
|   | 595 |     |  | 600 |  | 605 |
| Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys |     |     |  |     |  |     |
|   | 610 |     |  | 615 |  | 620 |
| Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly |     |     |  |     |  |     |
|   | 625 |     |  | 630 |  | 635 |
|   |     |     |  | 635 |  | 640 |
| Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly |     |     |  |     |  |     |
|   | 645 |     |  | 650 |  | 655 |
| Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser |     |     |  |     |  |     |
|   | 660 |     |  | 665 |  | 670 |
| Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp |     |     |  |     |  |     |
|   | 675 |     |  | 680 |  | 685 |
| Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys |     |     |  |     |  |     |
|   | 690 |     |  | 695 |  | 700 |
| Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn |     |     |  |     |  |     |
|   | 705 |     |  | 710 |  | 715 |
|   |     |     |  | 715 |  | 720 |
| Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu |     |     |  |     |  |     |
|   | 725 |     |  | 730 |  | 735 |
| Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala |     |     |  |     |  |     |
|   | 740 |     |  | 745 |  | 750 |
| Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala |     |     |  |     |  |     |
|   | 755 |     |  | 760 |  | 765 |
| Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu |     |     |  |     |  |     |
|   | 770 |     |  | 775 |  | 780 |
| Leu Thr Arg Lys Ser Pro Gly Val Ser Met Asn Gly Leu Asp Leu Pro |     |     |  |     |  |     |
|   | 785 |     |  | 790 |  | 795 |
|   |     |     |  | 795 |  | 800 |
| Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe |     |     |  |     |  |     |
|   | 805 |     |  | 810 |  | 815 |
| Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu |     |     |  |     |  |     |
|   | 820 |     |  | 825 |  | 830 |
| Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala |     |     |  |     |  |     |
|   | 835 |     |  | 840 |  | 845 |
| Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro |     |     |  |     |  |     |
|   | 850 |     |  | 855 |  | 860 |

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val  
 865 870 875

<210> 1107

<211> 854

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_will\_amplicon

<400> 1107

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  
 225 230 235 240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp  
 245 250 255  
 Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu  
 260 265 270  
 Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu  
 275 280 285  
 Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala  
 290 295 300  
 Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile  
 305 310 315 320  
 Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu  
 325 330 335  
 Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln  
 340 345 350  
 Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu  
 355 360 365  
 Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile  
 370 375 380  
 Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu  
 385 390 395 400  
 Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val  
 405 410 415  
 Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys  
 420 425 430  
 Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser  
 435 440 445  
 Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala  
 450 455 460  
 Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr  
 465 470 475 480  
 Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile  
 485 490 495  
 Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr  
 500 505 510  
 Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met  
 515 520 525  
 Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly Gly Asp Val Glu Ala  
 530 535 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala  
 545 550 555 560  
 Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys  
 565 570 575  
 Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln  
 580 585 590  
 Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu  
 595 600 605  
 Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val  
 610 615 620  
 Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu  
 625 630 635 640  
 Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly  
 645 650 655  
 Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala  
 660 665 670  
 Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile  
 675 680 685  
 Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr  
 690 695 700  
 Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala  
 705 710 715 720  
 Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala  
 725 730 735  
 Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr  
 740 745 750  
 Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly  
 755 760 765  
 Val Ser Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val  
 770 775 780  
 Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp  
 785 790 795 800  
 Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu  
 805 810 815  
 His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val  
 820 825 830  
 Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser  
 835 840 845  
 Pro Gly Asp Asp Ile Val

850

&lt;210&gt; 1108

&lt;211&gt; 877

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;223&gt; Seq ID: rhg1\_a2704\_amplicon

&lt;400&gt; 1108

Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
 1 5 10 15

Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
 20 25 30

Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
 35 40 45

Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
 50 55 60

Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
 65 70 75 80

Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
 85 90 95

Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
 100 105 110

Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
 115 120 125

Gly Gly Trp Val Gly Ile Lys Cys Ala Lys Gly Gln Val Ile Val Ile  
 130 135 140

Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
 145 150 155 160

Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
 165 170 175

Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
 180 185 190

Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
 195 200 205

Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
 210 215 220

Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
 225 230 235 240

Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |  |  |
| His | Ser | Phe | Ser | Leu | Thr | Phe | Leu | Ser | Leu | Gln | Asn | Asn | Asn | Leu | Ser |  |  |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |  |  |
| Gly | Ser | Leu | Pro | Asn | Ser | Trp | Gly | Gly | Asn | Ser | Lys | Asn | Gly | Phe | Phe |  |  |
|     |     |     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |  |  |
| Arg | Leu | Gln | Asn | Leu | Ile | Leu | Asp | His | Asn | Phe | Phe | Thr | Gly | Asp | Val |  |  |
|     |     |     | 290 |     |     |     |     |     | 295 |     |     |     |     |     | 300 |  |  |
| Pro | Ala | Ser | Leu | Gly | Ser | Leu | Arg | Glu | Leu | Asn | Glu | Ile | Ser | Leu | Ser |  |  |
| 305 |     |     |     |     |     | 310 |     |     |     |     |     | 315 |     |     | 320 |  |  |
| His | Asn | Lys | Phe | Ser | Gly | Ala | Ile | Pro | Asn | Glu | Ile | Gly | Thr | Leu | Ser |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     | 335 |  |  |
| Arg | Leu | Lys | Thr | Leu | Asp | Ile | Ser | Asn | Asn | Ala | Leu | Asn | Gly | Asn | Leu |  |  |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     | 350 |  |  |
| Pro | Ala | Thr | Leu | Ser | Asn | Leu | Ser | Ser | Leu | Thr | Leu | Leu | Asn | Ala | Glu |  |  |
|     |     |     | 355 |     |     |     |     |     | 360 |     |     |     |     |     | 365 |  |  |
| Asn | Asn | Leu | Leu | Asp | Asn | Gln | Ile | Pro | Gln | Ser | Leu | Gly | Arg | Leu | Arg |  |  |
| 370 |     |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |  |  |
| Asn | Leu | Ser | Val | Leu | Ile | Leu | Ser | Arg | Asn | Gln | Phe | Ser | Gly | His | Ile |  |  |
| 385 |     |     |     |     |     | 390 |     |     |     |     |     | 395 |     |     | 400 |  |  |
| Pro | Ser | Ser | Ile | Ala | Asn | Ile | Ser | Ser | Leu | Arg | Gln | Leu | Asp | Leu | Ser |  |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     |     | 415 |  |  |
| Leu | Asn | Asn | Phe | Ser | Gly | Glu | Ile | Pro | Val | Ser | Phe | Asp | Ser | Gln | Arg |  |  |
|     |     |     | 420 |     |     |     |     |     | 425 |     |     |     |     |     | 430 |  |  |
| Ser | Leu | Asn | Leu | Phe | Asn | Val | Ser | Tyr | Asn | Ser | Leu | Ser | Gly | Ser | Val |  |  |
|     |     |     | 435 |     |     |     |     |     | 440 |     |     |     |     |     | 445 |  |  |
| Pro | Pro | Leu | Leu | Ala | Lys | Lys | Phe | Asn | Ser | Ser | Ser | Phe | Val | Gly | Asn |  |  |
| 450 |     |     |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |  |  |
| Ile | Gln | Leu | Cys | Gly | Tyr | Ser | Pro | Ser | Thr | Pro | Cys | Leu | Ser | Gln | Ala |  |  |
| 465 |     |     |     |     |     | 470 |     |     |     |     |     | 475 |     |     | 480 |  |  |
| Pro | Ser | Gln | Gly | Val | Ile | Ala | Pro | Pro | Pro | Glu | Val | Ser | Lys | His | His |  |  |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     |     | 495 |  |  |
| His | His | Arg | Lys | Leu | Ser | Thr | Lys | Asp | Ile | Ile | Leu | Ile | Val | Ala | Gly |  |  |
|     |     |     | 500 |     |     |     |     |     | 505 |     |     |     |     |     | 510 |  |  |
| Val | Leu | Leu | Val | Val | Leu | Ile | Ile | Leu | Cys | Cys | Val | Leu | Leu | Phe | Cys |  |  |
|     |     |     | 515 |     |     |     |     |     | 520 |     |     |     |     |     | 525 |  |  |
| Leu | Ile | Arg | Lys | Arg | Ser | Thr | Ser | Lys | Ala | Gly | Asn | Gly | Gln | Ala | Thr |  |  |
| 530 |     |     |     |     |     | 535 |     |     |     |     |     | 540 |     |     |     |  |  |
| Glu | Gly | Arg | Ala | Ala | Thr | Met | Arg | Thr | Glu | Lys | Gly | Val | Pro | Pro | Val |  |  |
| 545 |     |     |     |     |     | 550 |     |     |     |     |     | 555 |     |     | 560 |  |  |

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val  
 565 570 575  
 His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala  
 580 585 590  
 Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala  
 595 600 605  
 Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys  
 610 615 620  
 Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly  
 625 630 635 640  
 Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly  
 645 650 655  
 Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser  
 660 665 670  
 Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp  
 675 680 685  
 Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys  
 690 695 700  
 Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn  
 705 710 715 720  
 Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu  
 725 730 735  
 Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala  
 740 745 750  
 Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala  
 755 760 765  
 Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu  
 770 775 780  
 Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro  
 785 790 795 800  
 Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe  
 805 810 815  
 Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu  
 820 825 830  
 Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala  
 835 840 845  
 Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro  
 850 855 860



Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val  
 865 870 875

<210> 1109

<211> 854

<212> PRT

<213> Glycine max

<223> Seq ID: rhg1\_a2704\_amplicon

<400> 1109

Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15

Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30

Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45

Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60

Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80

Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95

Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110

Cys Ala Lys Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125

Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140

Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160

Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175

Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190

Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205

Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220

Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  
 225 230 235 240

Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp  
 245 250 255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu  
 260 265 270

Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu  
 275 280 285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala  
 290 295 300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile  
 305 310 315 320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu  
 325 330 335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln  
 340 345 350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu  
 355 360 365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile  
 370 375 380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu  
 385 390 395 400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val  
 405 410 415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys  
 420 425 430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser  
 435 440 445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala  
 450 455 460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr  
 465 470 475 480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile  
 485 490 495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr  
 500 505 510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met  
 515 520 525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala  
 530 535 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala

|                     |   |     |     |     |     |     |
|---------------------|---|-----|-----|-----|-----|-----|
| 545                 |   | 550 |     | 555 |     | 560 |
| Phe Thr Ala Asp     | Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys |     |     |     |     |     |
|                     | 565   |     | 570 |     | 575 |     |
| Ser Thr Tyr Gly     | Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln |     |     |     |     |     |
|                     | 580   |     | 585 |     | 590 |     |
| Val Ala Val Lys Arg | Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu     |     |     |     |     |     |
|                     | 595   |     | 600 |     | 605 |     |
| Phe Glu Ser Glu Val | Ser Val Leu Gly Lys Ile Arg His Pro Asn Val     |     |     |     |     |     |
|                     | 610   |     | 615 |     | 620 |     |
| Leu Ala Leu Arg Ala | Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu     |     |     |     |     |     |
|                     | 625   |     | 630 |     | 635 |     |
| Val Phe Asp Tyr Met | Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly     |     |     |     |     |     |
|                     | 645   |     | 650 |     | 655 |     |
| Gly Gly Thr Glu Thr | Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala     |     |     |     |     |     |
|                     | 660   |     | 665 |     | 670 |     |
| Gln Asp Leu Ala Arg | Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile     |     |     |     |     |     |
|                     | 675   |     | 680 |     | 685 |     |
| Ile His Gly Asn Leu | Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr     |     |     |     |     |     |
|                     | 690   |     | 695 |     | 700 |     |
| Asn Ala Lys Ile Ala | Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala     |     |     |     |     |     |
|                     | 705   |     | 710 |     | 715 |     |
| Ala Asn Ser Asn Val | Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala     |     |     |     |     |     |
|                     | 725   |     | 730 |     | 735 |     |
| Pro Glu Leu Ser Lys | Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr     |     |     |     |     |     |
|                     | 740   |     | 745 |     | 750 |     |
| Ser Leu Gly Val Ile | Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly     |     |     |     |     |     |
|                     | 755   |     | 760 |     | 765 |     |
| Val Pro Met Asn Gly | Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val     |     |     |     |     |     |
|                     | 770   |     | 775 |     | 780 |     |
| Lys Glu Glu Trp Thr | Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp     |     |     |     |     |     |
|                     | 785   |     | 790 |     | 795 |     |
| Ala Ser Thr Val Gly | Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu     |     |     |     |     |     |
|                     | 805   |     | 810 |     | 815 |     |
| His Cys Val Asp Pro | Ser Pro Ser Ala Arg Pro Glu Val His Gln Val     |     |     |     |     |     |
|                     | 820   |     | 825 |     | 830 |     |
| Leu Gln Gln Leu Glu | Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser     |     |     |     |     |     |
|                     | 835   |     | 840 |     | 845 |     |
| Pro Gly Asp Asp Ile | Val   |     |     |     |     |     |
|                     | 850   |     |     |     |     |     |

<210> 1110  
 <211> 877  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: rhg1\_noir\_amplicon  
  
 <400> 1110  
  
 Met Asp Ala Tyr Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
 1 5 10 15  
  
 Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
 20 25 30  
  
 Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
 35 40 45  
  
 Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
 50 55 60  
  
 Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
 65 70 75 80  
  
 Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
 85 90 95  
  
 Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
 100 105 110  
  
 Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
 115 120 125  
  
 Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile  
 130 135 140  
  
 Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
 145 150 155 160  
  
 Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
 165 170 175  
  
 Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
 180 185 190  
  
 Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
 195 200 205  
  
 Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
 210 215 220  
  
 Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
 225 230 235 240  
  
 Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr  
 245 250 255

|   |     |     |     |
|---|-----|-----|-----|
| His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser | 260 | 265 | 270 |
| Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe | 275 | 280 | 285 |
| Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val | 290 | 295 | 300 |
| Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser | 305 | 310 | 315 |
| His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser | 325 | 330 | 335 |
| Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu | 340 | 345 | 350 |
| Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu | 355 | 360 | 365 |
| Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg | 370 | 375 | 380 |
| Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile | 385 | 390 | 395 |
| Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser | 405 | 410 | 415 |
| Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg | 420 | 425 | 430 |
| Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val | 435 | 440 | 445 |
| Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn | 450 | 455 | 460 |
| Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala | 465 | 470 | 475 |
| Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His | 485 | 490 | 495 |
| His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly | 500 | 505 | 510 |
| Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys | 515 | 520 | 525 |
| Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr | 530 | 535 | 540 |
| Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val | 545 | 550 | 555 |
|   |     |     | 560 |

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val  
565 570 575

His Phe Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala  
580 585 590

Thr Ala Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala  
595 600 605

Ile Leu Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys  
610 615 620

Ile Thr Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly  
625 630 635 640

Lys Ile Arg His Pro Asn Val Leu Ala Leu Arg Ala Tyr Tyr Leu Gly  
645 650 655

Pro Lys Gly Glu Lys Leu Leu Val Phe Asp Tyr Met Ser Lys Gly Ser  
660 665 670

Leu Ala Ser Phe Leu His Gly Gly Gly Thr Glu Thr Phe Ile Asp Trp  
675 680 685

Pro Thr Arg Met Lys Ile Ala Gln Asp Leu Ala Arg Gly Leu Phe Cys  
690 695 700

Leu His Ser Gln Glu Asn Ile Ile His Gly Asn Leu Thr Ser Ser Asn  
705 710 715 720

Val Leu Leu Asp Glu Asn Thr Asn Ala Lys Ile Ala Asp Phe Gly Leu  
725 730 735

Ser Arg Leu Met Ser Thr Ala Ala Asn Ser Asn Val Ile Ala Thr Ala  
740 745 750

Gly Ala Leu Gly Tyr Arg Ala Pro Glu Leu Ser Lys Leu Lys Lys Ala  
755 760 765

Asn Thr Lys Thr Asp Ile Tyr Ser Leu Gly Val Ile Leu Leu Glu Leu  
770 775 780

Leu Thr Arg Lys Ser Pro Gly Val Pro Met Asn Gly Leu Asp Leu Pro  
785 790 795 800

Gln Trp Val Ala Ser Val Val Lys Glu Glu Trp Thr Asn Glu Val Phe  
805 810 815

Asp Ala Asp Leu Met Arg Asp Ala Ser Thr Val Gly Asp Glu Leu Leu  
820 825 830

Asn Thr Leu Lys Leu Ala Leu His Cys Val Asp Pro Ser Pro Ser Ala  
835 840 845

Arg Pro Glu Val His Gln Val Leu Gln Gln Leu Glu Glu Ile Arg Pro  
850 855 860

Glu Arg Ser Val Thr Ala Ser Pro Gly Asp Asp Ile Val

|       |     |                            |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
|-------|-----|----------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|
| 865   | 870 |                            |     |     |     |     |     |     |     |     |     |     |     | 875 |     |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <210> |     | 1111                       |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <211> |     | 854                        |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <212> |     | PRT                        |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <213> |     | Glycine max                |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <223> |     | Seq ID: rhg1_noir_amplicon |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| <400> |     | 1111                       |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Met   | Val | Val                        | Ala | Val | Glu | Lys | Thr | Asn | Leu | Thr | Ser | Gln | Ser | Gln | Cys |  |  |  |  |  |  |  |  |  |  |  |  |
| 1     |     |                            |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Phe   | Asn | Arg                        | Val | Ser | Asp | Lys | Lys | Lys | Glu | Arg | Cys | Lys | Thr | His | Met |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Asn   | Asn | Val                        | Asn | Pro | Cys | Cys | Phe | Leu | Phe | Leu | Leu | Cys | Val | Trp | Ser |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     | 35                         |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu   | Val | Val                        | Leu | Pro | Ser | Cys | Val | Arg | Pro | Val | Leu | Cys | Glu | Asp | Glu |  |  |  |  |  |  |  |  |  |  |  |  |
|       | 50  |                            |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly   | Trp | Asp                        | Gly | Val | Val | Val | Thr | Ala | Ser | Asn | Leu | Leu | Ala | Leu | Glu |  |  |  |  |  |  |  |  |  |  |  |  |
| 65    |     |                            |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ala   | Phe | Lys                        | Gln | Glu | Leu | Val | Asp | Pro | Glu | Gly | Phe | Leu | Arg | Ser | Trp |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Asn   | Asp | Ser                        | Gly | Tyr | Gly | Ala | Cys | Ser | Gly | Gly | Trp | Val | Gly | Ile | Lys |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Cys   | Ala | Gln                        | Gly | Gln | Val | Ile | Val | Ile | Gln | Leu | Pro | Trp | Lys | Gly | Leu |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     | 115                        |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Arg   | Gly | Arg                        | Ile | Thr | Asp | Lys | Ile | Gly | Gln | Leu | Gln | Gly | Leu | Arg | Lys |  |  |  |  |  |  |  |  |  |  |  |  |
|       | 130 |                            |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu   | Ser | Leu                        | His | Asp | Asn | Gln | Ile | Gly | Gly | Ser | Ile | Pro | Ser | Thr | Leu |  |  |  |  |  |  |  |  |  |  |  |  |
| 145   |     |                            |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly   | Leu | Leu                        | Pro | Asn | Leu | Arg | Gly | Val | Gln | Leu | Phe | Asn | Asn | Arg | Leu |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Thr   | Gly | Ser                        | Ile | Pro | Leu | Ser | Leu | Gly | Phe | Cys | Pro | Leu | Leu | Gln | Ser |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     |                            | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu   | Asp | Leu                        | Ser | Asn | Asn | Leu | Leu | Thr | Gly | Ala | Ile | Pro | Tyr | Ser | Leu |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     | 195                        |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Ala   | Asn | Ser                        | Thr | Lys | Leu | Tyr | Trp | Leu | Asn | Leu | Ser | Phe | Asn | Ser | Phe |  |  |  |  |  |  |  |  |  |  |  |  |
|       |     | 210                        |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
| Ser   | Gly | Pro                        | Leu | Pro | Ala | Ser | Leu | Thr | His | Ser | Phe | Ser | Leu | Thr | Phe |  |  |  |  |  |  |  |  |  |  |  |  |
| 225   |     |                            |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu   | Ser | Leu                        | Gln | Asn | Asn | Asn | Leu | Ser | Gly | Ser | Leu | Pro | Asn | Ser | Trp |  |  |  |  |  |  |  |  |  |  |  |  |

|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
|   | 245 |     | 250 |     | 255 |
| Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu |     |     |     |     |     |
|   | 260 |     | 265 |     | 270 |
| Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu |     |     |     |     |     |
|   | 275 |     | 280 |     | 285 |
| Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala |     |     |     |     |     |
|   | 290 |     | 295 |     | 300 |
| Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile |     |     |     |     |     |
| 305   |     | 310 |     | 315 | 320 |
| Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu |     |     |     |     |     |
|   | 325 |     | 330 |     | 335 |
| Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln |     |     |     |     |     |
|   | 340 |     | 345 |     | 350 |
| Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu |     |     |     |     |     |
|   | 355 |     | 360 |     | 365 |
| Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile |     |     |     |     |     |
|   | 370 |     | 375 |     | 380 |
| Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu |     |     |     |     |     |
| 385   |     | 390 |     | 395 | 400 |
| Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val |     |     |     |     |     |
|   | 405 |     | 410 |     | 415 |
| Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys |     |     |     |     |     |
|   | 420 |     | 425 |     | 430 |
| Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser |     |     |     |     |     |
|   | 435 |     | 440 |     | 445 |
| Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala |     |     |     |     |     |
|   | 450 |     | 455 |     | 460 |
| Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr |     |     |     |     |     |
| 465   |     | 470 |     | 475 | 480 |
| Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile |     |     |     |     |     |
|   | 485 |     | 490 |     | 495 |
| Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr |     |     |     |     |     |
|   | 500 |     | 505 |     | 510 |
| Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met |     |     |     |     |     |
|   | 515 |     | 520 |     | 525 |
| Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala |     |     |     |     |     |
|   | 530 |     | 535 |     | 540 |
| Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala |     |     |     |     |     |
| 545   |     | 550 |     | 555 | 560 |



Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys  
 565 570 575  
 Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln  
 580 585 590  
 Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu  
 595 600 605  
 Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val  
 610 615 620  
 Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu  
 625 630 635 640  
 Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly  
 645 650 655  
 Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala  
 660 665 670  
 Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile  
 675 680 685  
 Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr  
 690 695 700  
 Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala  
 705 710 715 720  
 Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala  
 725 730 735  
 Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr  
 740 745 750  
 Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly  
 755 760 765  
 Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val  
 770 775 780  
 Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp  
 785 790 795 800  
 Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu  
 805 810 815  
 His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val  
 820 825 830  
 Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser  
 835 840 845  
 Pro Gly Asp Asp Ile Val  
 850

<210> 1112  
 <211> 877  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: rhg1\_lee\_amplicon  
  
 <400> 1112  
  
 Met Asp Ala Tyr Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
 1 5 10 15  
  
 Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
 20 25 30  
  
 Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
 35 40 45  
  
 Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
 50 55 60  
  
 Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
 65 70 75 80  
  
 Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
 85 90 95  
  
 Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
 100 105 110  
  
 Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
 115 120 125  
  
 Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile  
 130 135 140  
  
 Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
 145 150 155 160  
  
 Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
 165 170 175  
  
 Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
 180 185 190  
  
 Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
 195 200 205  
  
 Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
 210 215 220  
  
 Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
 225 230 235 240  
  
 Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr  
 245 250 255

His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser  
 260 265 270

Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe  
 275 280 285

Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val  
 290 295 300

Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser  
 305 310 315 320

His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser  
 325 330 335

Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu  
 340 345 350

Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu  
 355 360 365

Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg  
 370 375 380

Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile  
 385 390 395 400

Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser  
 405 410 415

Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg  
 420 425 430

Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val  
 435 440 445

Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn  
 450 455 460

Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala  
 465 470 475 480

Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His  
 485 490 495

His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly  
 500 505 510

Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys  
 515 520 525

Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr  
 530 535 540

Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val  
 545 550 555 560

Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 565 |     |     |     |     |     |     |     |     |     | 570 |     |     |     |     | 575 |  |  |  |  |
| His | Phe | Asp | Gly | Pro | Met | Ala | Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala |  |  |  |  |
|     |     |     | 580 |     |     |     |     |     | 585 |     |     |     | 590 |     |     |  |  |  |  |
| Thr | Ala | Glu | Ile | Met | Gly | Lys | Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala |  |  |  |  |
|     |     |     | 595 |     |     |     |     |     | 600 |     |     |     | 605 |     |     |  |  |  |  |
| Ile | Leu | Glu | Asp | Gly | Ser | Gln | Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys |  |  |  |  |
|     |     |     | 610 |     |     |     |     |     | 615 |     |     |     | 620 |     |     |  |  |  |  |
| Ile | Thr | Lys | Gly | His | Arg | Glu | Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly |  |  |  |  |
|     |     |     | 625 |     |     |     |     |     | 630 |     |     |     | 635 |     |     |  |  |  |  |
| Lys | Ile | Arg | His | Pro | Asn | Val | Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly |  |  |  |  |
|     |     |     | 645 |     |     |     |     |     | 650 |     |     |     | 655 |     |     |  |  |  |  |
| Pro | Lys | Gly | Glu | Lys | Leu | Leu | Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser |  |  |  |  |
|     |     |     | 660 |     |     |     |     |     | 665 |     |     |     | 670 |     |     |  |  |  |  |
| Leu | Ala | Ser | Phe | Leu | His | Gly | Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp |  |  |  |  |
|     |     |     | 675 |     |     |     |     |     | 680 |     |     |     | 685 |     |     |  |  |  |  |
| Pro | Thr | Arg | Met | Lys | Ile | Ala | Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys |  |  |  |  |
|     |     |     | 690 |     |     |     |     |     | 695 |     |     |     | 700 |     |     |  |  |  |  |
| Leu | His | Ser | Gln | Glu | Asn | Ile | Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn |  |  |  |  |
|     |     |     | 705 |     |     |     |     |     | 710 |     |     |     | 715 |     |     |  |  |  |  |
| Val | Leu | Leu | Asp | Glu | Asn | Thr | Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu |  |  |  |  |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     | 735 |     |     |  |  |  |  |
| Ser | Arg | Leu | Met | Ser | Thr | Ala | Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala |  |  |  |  |
|     |     |     | 740 |     |     |     |     |     | 745 |     |     |     | 750 |     |     |  |  |  |  |
| Gly | Ala | Leu | Gly | Tyr | Arg | Ala | Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala |  |  |  |  |
|     |     |     | 755 |     |     |     |     |     | 760 |     |     |     | 765 |     |     |  |  |  |  |
| Asn | Thr | Lys | Thr | Asp | Ile | Tyr | Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu |  |  |  |  |
|     |     |     | 770 |     |     |     |     |     | 775 |     |     |     | 780 |     |     |  |  |  |  |
| Leu | Thr | Arg | Lys | Ser | Pro | Gly | Val | Pro | Met | Asn | Gly | Leu | Asp | Leu | Pro |  |  |  |  |
|     |     |     | 785 |     |     |     |     |     | 790 |     |     |     | 795 |     |     |  |  |  |  |
| Gln | Trp | Val | Ala | Ser | Val | Val | Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe |  |  |  |  |
|     |     |     | 805 |     |     |     |     |     | 810 |     |     |     | 815 |     |     |  |  |  |  |
| Asp | Ala | Asp | Leu | Met | Arg | Asp | Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu |  |  |  |  |
|     |     |     | 820 |     |     |     |     |     | 825 |     |     |     | 830 |     |     |  |  |  |  |
| Asn | Thr | Leu | Lys | Leu | Ala | Leu | His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala |  |  |  |  |
|     |     |     | 835 |     |     |     |     |     | 840 |     |     |     | 845 |     |     |  |  |  |  |
| Arg | Pro | Glu | Val | His | Gln | Val | Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro |  |  |  |  |
|     |     |     | 850 |     |     |     |     |     | 855 |     |     |     | 860 |     |     |  |  |  |  |
| Glu | Arg | Ser | Val | Thr | Ala | Ser | Pro | Gly | Asp | Asp | Ile | Val |     |     |     |  |  |  |  |
|     |     |     | 865 |     |     |     |     |     | 870 |     |     |     | 875 |     |     |  |  |  |  |

<210> 1113  
 <211> 854  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: rhg1\_lee\_amplicon  
  
 <400> 1113  
  
 Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15  
  
 Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30  
  
 Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45  
  
 Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60  
  
 Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80  
  
 Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95  
  
 Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110  
  
 Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125  
  
 Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140  
  
 Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160  
  
 Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175  
  
 Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190  
  
 Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205  
  
 Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220  
  
 Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  
 225 230 235 240  
  
 Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp  
 245 250 255

Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu  
 260 265 270

Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu  
 275 280 285

Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala  
 290 295 300

Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile  
 305 310 315 320

Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu  
 325 330 335

Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln  
 340 345 350

Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu  
 355 360 365

Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile  
 370 375 380

Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu  
 385 390 395 400

Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val  
 405 410 415

Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys  
 420 425 430

Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser  
 435 440 445

Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala  
 450 455 460

Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr  
 465 470 475 480

Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile  
 485 490 495

Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr  
 500 505 510

Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met  
 515 520 525

Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala  
 530 535 540

Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala  
 545 550 555 560

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys  
 565 570 575  
 Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln  
 580 585 590  
 Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu  
 595 600 605  
 Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val  
 610 615 620  
 Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu  
 625 630 635 640  
 Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly  
 645 650 655  
 Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala  
 660 665 670  
 Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile  
 675 680 685  
 Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr  
 690 695 700  
 Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala  
 705 710 715 720  
 Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala  
 725 730 735  
 Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr  
 740 745 750  
 Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly  
 755 760 765  
 Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val  
 770 775 780  
 Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp  
 785 790 795 800  
 Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu  
 805 810 815  
 His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val  
 820 825 830  
 Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser  
 835 840 845  
 Pro Gly Asp Asp Ile Val  
 850

<210> 1114  
 <211> 877  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: rhgl\_pi200499\_amplicon  
  
 <400> 1114  
  
 Met Asp Ala Cys Gly Met Ser Ser Ser Asn Ser Lys His Val Val Asp  
 1 5 10 15  
  
 Gln Lys Arg Ser Thr Met Asn Met Met Ile Thr Thr Ile Leu Leu Arg  
 20 25 30  
  
 Phe Trp Asp Arg Tyr Asp Met Asn Cys Asp Tyr Thr Thr Asn Ser Tyr  
 35 40 45  
  
 Glu Pro Gly Thr Gln Leu Ala Pro Ser Ser Pro Arg Asp Thr Ser Val  
 50 55 60  
  
 Lys Leu Gly Asp Ala Ser Ser Leu Val Val Leu Pro Ser Cys Val Arg  
 65 70 75 80  
  
 Pro Val Leu Cys Glu Asp Glu Gly Trp Asp Gly Val Val Val Thr Ala  
 85 90 95  
  
 Ser Asn Leu Leu Ala Leu Glu Ala Phe Lys Gln Glu Leu Val Asp Pro  
 100 105 110  
  
 Glu Gly Phe Leu Arg Ser Trp Asn Asp Ser Gly Tyr Gly Ala Cys Ser  
 115 120 125  
  
 Gly Gly Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile  
 130 135 140  
  
 Gln Leu Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly  
 145 150 155 160  
  
 Gln Leu Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly  
 165 170 175  
  
 Gly Ser Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val  
 180 185 190  
  
 Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly  
 195 200 205  
  
 Phe Cys Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr  
 210 215 220  
  
 Gly Ala Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu  
 225 230 235 240  
  
 Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr  
 245 250 255



His Ser Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser  
 260 265 270  
 Gly Ser Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe  
 275 280 285  
 Arg Leu Gln Asn Leu Ile Leu Asp Asn Asn Phe Phe Thr Gly Asp Val  
 290 295 300  
 Pro Ala Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser  
 305 310 315 320  
 His Asn Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser  
 325 330 335  
 Arg Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu  
 340 345 350  
 Pro Ala Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu  
 355 360 365  
 Asn Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg  
 370 375 380  
 Asn Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile  
 385 390 395 400  
 Pro Ser Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser  
 405 410 415  
 Leu Asn Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg  
 420 425 430  
 Ser Leu Asn Leu Phe Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val  
 435 440 445  
 Pro Pro Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn  
 450 455 460  
 Ile Gln Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala  
 465 470 475 480  
 Pro Ser Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His  
 485 490 495  
 His His Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly  
 500 505 510  
 Val Leu Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys  
 515 520 525  
 Leu Ile Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr  
 530 535 540  
 Glu Gly Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val  
 545 550 555 560  
 Ala Ala Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| His | Phe | Asp | Gly | Pro | Met | Ala | Phe | Thr | Ala | Asp | Asp | Leu | Leu | Cys | Ala |
|     |     |     | 580 |     |     |     |     |     | 585 |     |     |     | 590 |     |     |
| Thr | Ala | Glu | Ile | Met | Gly | Lys | Ser | Thr | Tyr | Gly | Thr | Val | Tyr | Lys | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ile | Leu | Glu | Asp | Gly | Ser | Gln | Val | Ala | Val | Lys | Arg | Leu | Arg | Glu | Lys |
|     |     | 610 |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ile | Thr | Lys | Gly | His | Arg | Glu | Phe | Glu | Ser | Glu | Val | Ser | Val | Leu | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     | 640 |     |
| Lys | Ile | Arg | His | Pro | Asn | Val | Leu | Ala | Leu | Arg | Ala | Tyr | Tyr | Leu | Gly |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Pro | Lys | Gly | Glu | Lys | Leu | Leu | Val | Phe | Asp | Tyr | Met | Ser | Lys | Gly | Ser |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Leu | Ala | Ser | Phe | Leu | His | Gly | Gly | Gly | Thr | Glu | Thr | Phe | Ile | Asp | Trp |
|     |     | 675 |     |     |     | 680 |     |     |     |     |     | 685 |     |     |     |
| Pro | Thr | Arg | Met | Lys | Ile | Ala | Gln | Asp | Leu | Ala | Arg | Gly | Leu | Phe | Cys |
|     |     | 690 |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Leu | His | Ser | Gln | Glu | Asn | Ile | Ile | His | Gly | Asn | Leu | Thr | Ser | Ser | Asn |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Val | Leu | Leu | Asp | Glu | Asn | Thr | Asn | Ala | Lys | Ile | Ala | Asp | Phe | Gly | Leu |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     | 735 |     |     |
| Ser | Arg | Leu | Met | Ser | Thr | Ala | Ala | Asn | Ser | Asn | Val | Ile | Ala | Thr | Ala |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Gly | Ala | Leu | Gly | Tyr | Arg | Ala | Pro | Glu | Leu | Ser | Lys | Leu | Lys | Lys | Ala |
|     |     | 755 |     |     |     | 760 |     |     |     |     |     | 765 |     |     |     |
| Asn | Thr | Lys | Thr | Asp | Ile | Tyr | Ser | Leu | Gly | Val | Ile | Leu | Leu | Glu | Leu |
|     |     | 770 |     |     | 775 |     |     |     |     |     | 780 |     |     |     |     |
| Leu | Thr | Arg | Lys | Ser | Pro | Gly | Val | Pro | Met | Asn | Gly | Leu | Asp | Leu | Pro |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |
| Gln | Trp | Val | Ala | Ser | Val | Val | Lys | Glu | Glu | Trp | Thr | Asn | Glu | Val | Phe |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     | 815 |     |     |
| Asp | Ala | Asp | Leu | Met | Arg | Asp | Ala | Ser | Thr | Val | Gly | Asp | Glu | Leu | Leu |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Asn | Thr | Leu | Lys | Leu | Ala | Leu | His | Cys | Val | Asp | Pro | Ser | Pro | Ser | Ala |
|     |     | 835 |     |     |     | 840 |     |     |     |     |     | 845 |     |     |     |
| Arg | Pro | Glu | Val | His | Gln | Val | Leu | Gln | Gln | Leu | Glu | Glu | Ile | Arg | Pro |
|     |     | 850 |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |
| Glu | Arg | Ser | Val | Thr | Ala | Ser | Pro | Gly | Asp | Asp | Ile | Val |     |     |     |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     |     |

<210> 1115  
 <211> 854  
 <212> PRT  
 <213> Glycine max  
  
 <223> Seq ID: rhgl\_pi200499\_amplicon  
  
 <400> 1115  
  
 Met Val Val Ala Val Glu Lys Thr Asn Leu Thr Ser Gln Ser Gln Cys  
 1 5 10 15  
  
 Phe Asn Arg Val Ser Asp Lys Lys Lys Glu Arg Cys Lys Thr His Met  
 20 25 30  
  
 Asn Asn Val Asn Pro Cys Cys Phe Leu Phe Leu Leu Cys Val Trp Ser  
 35 40 45  
  
 Leu Val Val Leu Pro Ser Cys Val Arg Pro Val Leu Cys Glu Asp Glu  
 50 55 60  
  
 Gly Trp Asp Gly Val Val Val Thr Ala Ser Asn Leu Leu Ala Leu Glu  
 65 70 75 80  
  
 Ala Phe Lys Gln Glu Leu Val Asp Pro Glu Gly Phe Leu Arg Ser Trp  
 85 90 95  
  
 Asn Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly Trp Val Gly Ile Lys  
 100 105 110  
  
 Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu Pro Trp Lys Gly Leu  
 115 120 125  
  
 Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu Gln Gly Leu Arg Lys  
 130 135 140  
  
 Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser Ile Pro Ser Thr Leu  
 145 150 155 160  
  
 Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu Phe Asn Asn Arg Leu  
 165 170 175  
  
 Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys Pro Leu Leu Gln Ser  
 180 185 190  
  
 Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala Ile Pro Tyr Ser Leu  
 195 200 205  
  
 Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu Ser Phe Asn Ser Phe  
 210 215 220  
  
 Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser Phe Ser Leu Thr Phe  
 225 230 235 240  
  
 Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser Leu Pro Asn Ser Trp  
 245 250 255

|   |     |     |     |
|---|-----|-----|-----|
| Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu Gln Asn Leu Ile Leu | 260 | 265 | 270 |
| Asp Asn Asn Phe Phe Thr Gly Asp Val Pro Ala Ser Leu Gly Ser Leu | 275 | 280 | 285 |
| Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn Lys Phe Ser Gly Ala | 290 | 295 | 300 |
| Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu Lys Thr Leu Asp Ile | 305 | 310 | 315 |
| Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala Thr Leu Ser Asn Leu | 325 | 330 | 335 |
| Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn Leu Leu Asp Asn Gln | 340 | 345 | 350 |
| Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu Ser Val Leu Ile Leu | 355 | 360 | 365 |
| Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser Ser Ile Ala Asn Ile | 370 | 375 | 380 |
| Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn Asn Phe Ser Gly Glu | 385 | 390 | 395 |
| Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu Asn Leu Phe Asn Val | 405 | 410 | 415 |
| Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro Leu Leu Ala Lys Lys | 420 | 425 | 430 |
| Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln Leu Cys Gly Tyr Ser | 435 | 440 | 445 |
| Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser Gln Gly Val Ile Ala | 450 | 455 | 460 |
| Pro Pro Pro Glu Val Ser Lys His His His His Arg Lys Leu Ser Thr | 465 | 470 | 475 |
| Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu Leu Val Val Leu Ile | 485 | 490 | 495 |
| Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile Arg Lys Arg Ser Thr | 500 | 505 | 510 |
| Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly Arg Ala Ala Thr Met | 515 | 520 | 525 |
| Arg Thr Glu Lys Gly Val Pro Pro Val Ala Ala Gly Asp Val Glu Ala | 530 | 535 | 540 |
| Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe Asp Gly Pro Met Ala | 545 | 550 | 555 |
|   |     |     | 560 |

Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala Glu Ile Met Gly Lys  
 565 570 575  
 Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu Glu Asp Gly Ser Gln  
 580 585 590  
 Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr Lys Gly His Arg Glu  
 595 600 605  
 Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile Arg His Pro Asn Val  
 610 615 620  
 Leu Ala Leu Arg Ala Tyr Tyr Leu Gly Pro Lys Gly Glu Lys Leu Leu  
 625 630 635 640  
 Val Phe Asp Tyr Met Ser Lys Gly Ser Leu Ala Ser Phe Leu His Gly  
 645 650 655  
 Gly Gly Thr Glu Thr Phe Ile Asp Trp Pro Thr Arg Met Lys Ile Ala  
 660 665 670  
 Gln Asp Leu Ala Arg Gly Leu Phe Cys Leu His Ser Gln Glu Asn Ile  
 675 680 685  
 Ile His Gly Asn Leu Thr Ser Ser Asn Val Leu Leu Asp Glu Asn Thr  
 690 695 700  
 Asn Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Leu Met Ser Thr Ala  
 705 710 715 720  
 Ala Asn Ser Asn Val Ile Ala Thr Ala Gly Ala Leu Gly Tyr Arg Ala  
 725 730 735  
 Pro Glu Leu Ser Lys Leu Lys Lys Ala Asn Thr Lys Thr Asp Ile Tyr  
 740 745 750  
 Ser Leu Gly Val Ile Leu Leu Glu Leu Leu Thr Arg Lys Ser Pro Gly  
 755 760 765  
 Val Pro Met Asn Gly Leu Asp Leu Pro Gln Trp Val Ala Ser Val Val  
 770 775 780  
 Lys Glu Glu Trp Thr Asn Glu Val Phe Asp Ala Asp Leu Met Arg Asp  
 785 790 795 800  
 Ala Ser Thr Val Gly Asp Glu Leu Leu Asn Thr Leu Lys Leu Ala Leu  
 805 810 815  
 His Cys Val Asp Pro Ser Pro Ser Ala Arg Pro Glu Val His Gln Val  
 820 825 830  
 Leu Gln Gln Leu Glu Glu Ile Arg Pro Glu Arg Ser Val Thr Ala Ser  
 835 840 845  
 Pro Gly Asp Asp Ile Val  
 850

<210> 1116  
 <211> 894  
 <212> PRT  
 <213> Glycine max

<223> Seq ID: rhg4\_a3244\_amplicon

<400> 1116

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser  
 1 5 10 15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser  
 20 25 30

Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr  
 35 40 45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu  
 50 55 60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser  
 65 70 75 80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser  
 85 90 95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly  
 100 105 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser  
 115 120 125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly  
 130 135 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg  
 145 150 155 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala  
 165 170 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu  
 180 185 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser  
 195 200 205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln  
 210 215 220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly  
 225 230 235 240

Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser  
 245 250 255

Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 260 |     |     |     |     |     |     |     |     |     | 265 |     |     |     |     | 270 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Val | Asn | Val | Thr | Leu | Asp | Gly | Ile | Asn | Ser | Phe | Cys | Leu | Asp | Thr | Pro |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Asn | Cys | Asp | Pro | Arg | Val | Met | Val | Leu | Leu | Gln | Ile | Ala | Glu | Ala |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Phe | Gly | Tyr | Pro | Ile | Arg | Leu | Ala | Glu | Ser | Trp | Lys | Gly | Asn | Asp | Pro |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Cys | Asp | Gly | Trp | Asn | Tyr | Val | Val | Cys | Ala | Ala | Gly | Lys | Ile | Ile | Thr |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Val | Asn | Phe | Glu | Lys | Gln | Gly | Leu | Gln | Gly | Thr | Ile | Ser | Pro | Ala | Phe |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ala | Asn | Leu | Thr | Asp | Leu | Arg | Thr | Leu | Phe | Leu | Asn | Gly | Asn | Asn | Leu |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ile | Gly | Ser | Ile | Pro | Asp | Ser | Leu | Ile | Thr | Leu | Pro | Gln | Leu | Gln | Thr |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Asp | Val | Ser | Asp | Asn | Asn | Leu | Ser | Gly | Leu | Val | Pro | Lys | Phe | Pro |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     | 400 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Pro | Lys | Val | Lys | Leu | Val | Thr | Ala | Gly | Asn | Ala | Leu | Leu | Gly | Lys | Pro |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Ser | Pro | Gly | Gly | Gly | Pro | Ser | Gly | Thr | Thr | Pro | Ser | Gly | Ser | Ser |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Thr | Gly | Gly | Ser | Gly | Gly | Glu | Ser | Ser | Lys | Gly | Asn | Ser | Ser | Val | Ser |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Pro | Gly | Trp | Ile | Ala | Gly | Ile | Val | Val | Ile | Val | Leu | Phe | Phe | Ile | Ala |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Val | Val | Leu | Phe | Val | Ser | Trp | Lys | Cys | Phe | Val | Asn | Lys | Leu | Gln | Gly |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     | 475 |     |     |     |     | 480 |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Lys | Phe | Ser | Arg | Val | Lys | Gly | His | Glu | Asn | Gly | Lys | Gly | Gly | Phe | Lys |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Asp | Ala | Val | His | Val | Ser | Asn | Gly | Tyr | Gly | Gly | Val | Pro | Val | Glu |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Gln | Ser | Gln | Ser | Ser | Gly | Asp | Arg | Ser | Asp | Leu | His | Ala | Leu | Asp |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Pro | Thr | Phe | Ser | Ile | Gln | Val | Leu | Arg | Gln | Val | Thr | Asn | Asn | Phe |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ser | Glu | Glu | Asn | Ile | Leu | Gly | Arg | Gly | Gly | Phe | Gly | Val | Val | Tyr | Lys |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Val | Leu | His | Asp | Gly | Thr | Lys | Ile | Ala | Val | Lys | Arg | Met | Glu | Ser |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     | 565 |     |     |     | 570 |     |     |     |     |     | 575 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ala | Met | Gly | Asn | Lys | Gly | Gln | Lys | Glu | Phe | Glu | Ala | Glu | Ile | Ala |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |
| Leu | Leu | Ser | Lys | Val | Arg | His | Arg | His | Leu | Val | Ala | Leu | Leu | Gly | Tyr |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |
| Cys | Ile | Asn | Gly | Asn | Glu | Arg | Leu | Leu | Val | Tyr | Glu | Tyr | Met | Pro | Gln |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |
| Gly | Thr | Leu | Thr | Gln | His | Leu | Phe | Glu | Trp | Gln | Glu | His | Gly | Tyr | Ala |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |
| Pro | Leu | Thr | Trp | Lys | Gln | Arg | Val | Val | Ile | Ala | Leu | Asp | Val | Ala | Arg |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |
| Gly | Val | Glu | Tyr | Leu | His | Ser | Leu | Ala | Gln | Gln | Ser | Phe | Ile | His | Arg |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |  |
| Asp | Leu | Lys | Pro | Ser | Asn | Ile | Leu | Leu | Gly | Asp | Asp | Met | Arg | Ala | Lys |  |
|     | 675 |     |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |
| Val | Ala | Asp | Phe | Gly | Leu | Val | Lys | Asn | Ala | Pro | Asp | Gly | Lys | Tyr | Ser |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |
| Val | Glu | Thr | Arg | Leu | Ala | Gly | Thr | Phe | Gly | Tyr | Leu | Ala | Pro | Glu | Tyr |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |
| Ala | Ala | Thr | Gly | Arg | Val | Thr | Thr | Lys | Val | Asp | Val | Tyr | Ala | Phe | Gly |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |
| Val | Val | Leu | Met | Glu | Leu | Ile | Thr | Gly | Arg | Lys | Ala | Leu | Asp | Asp | Thr |  |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |
| Val | Pro | Asp | Glu | Arg | Ser | His | Leu | Val | Thr | Trp | Phe | Arg | Arg | Val | Leu |  |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |
| Ile | Asn | Lys | Glu | Asn | Ile | Pro | Lys | Ala | Ile | Asp | Gln | Ile | Leu | Asn | Pro |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |
| Asp | Glu | Glu | Thr | Met | Gly | Ser | Ile | Tyr | Thr | Val | Ala | Glu | Leu | Ala | Gly |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |  |
| His | Cys | Thr | Ala | Arg | Glu | Pro | Tyr | Gln | Arg | Pro | Asp | Met | Gly | His | Ala |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |
| Val | Asn | Val | Leu | Val | Pro | Leu | Val | Glu | Gln | Trp | Lys | Pro | Thr | Ser | His |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |  |
| Asp | Glu | Glu | Glu | Glu | Asp | Gly | Ser | Gly | Gly | Asp | Leu | His | Met | Ser | Leu |  |
|     |     | 835 |     |     |     | 840 |     |     |     |     |     | 845 |     |     |     |  |
| Pro | Gln | Ala | Leu | Arg | Arg | Trp | Gln | Ala | Asn | Glu | Gly | Thr | Ser | Ser | Ile |  |
|     |     |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |  |
| Phe | Asn | Asp | Ile | Ser | Ile | Ser | Gln | Thr | Gln | Ser | Ser | Ile | Ser | Ser | Lys |  |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |  |



Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg  
                                   885                                  890

<210>          1117

<211>          894

<212>          PRT

<213>          Glycine max

<223>          Seq ID: rhg4\_Minsoy\_amplicon

<400>          1117

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser  
   1                          5                          10                          15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser  
                           20                          25                          30

Ser His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr  
                           35                          40                          45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu  
           50                          55                          60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser  
   65                          70                          75                          80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser  
                           85                          90                          95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly  
                           100                          105                          110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser  
           115                          120                          125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly  
           130                          135                          140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg  
   145                          150                          155                          160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala  
                           165                          170                          175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu  
                           180                          185                          190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser  
           195                          200                          205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln  
           210                          215                          220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly  
   225                          230                          235                          240

Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser  
 245 250 255  
 Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly  
 260 265 270  
 Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro  
 275 280 285  
 Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala  
 290 295 300  
 Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro  
 305 310 315 320  
 Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr  
 325 330 335  
 Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe  
 340 345 350  
 Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu  
 355 360 365  
 Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr  
 370 375 380  
 Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro  
 385 390 395 400  
 Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro  
 405 410 415  
 Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser  
 420 425 430  
 Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser  
 435 440 445  
 Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala  
 450 455 460  
 Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly  
 465 470 475 480  
 Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys  
 485 490 495  
 Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu  
 500 505 510  
 Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp  
 515 520 525  
 Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe  
 530 535 540  
 Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys

|                     |                     |                 |             |     |  |     |
|---------------------|---------------------|-----------------|-------------|-----|--|-----|
| 545                 |                     | 550             |             | 555 |  | 560 |
| Gly Val Leu His Asp | Gly Thr Lys Ile Ala | Val Lys Arg Met | Glu Ser     |     |  |     |
| 565                 | 570                 | 575             |             |     |  |     |
| Val Ala Met Gly Asn | Lys Gly Gln Lys Glu | Phe Glu Ala Glu | Ile Ala     |     |  |     |
| 580                 | 585                 | 590             |             |     |  |     |
| Leu Leu Ser Lys Val | Arg His Arg His     | Leu Val Ala Leu | Leu Gly Tyr |     |  |     |
| 595                 | 600                 | 605             |             |     |  |     |
| Cys Ile Asn Gly Asn | Glu Arg Leu Leu Val | Tyr Glu Tyr Met | Pro Gln     |     |  |     |
| 610                 | 615                 | 620             |             |     |  |     |
| Gly Thr Leu Thr Gln | His Leu Phe Glu Trp | Gln Glu His Gly | Tyr Ala     |     |  |     |
| 625                 | 630                 | 635             | 640         |     |  |     |
| Pro Leu Thr Trp Lys | Gln Arg Val Val Ile | Ala Leu Asp Val | Ala Arg     |     |  |     |
| 645                 | 650                 | 655             |             |     |  |     |
| Gly Val Glu Tyr Leu | His Ser Leu Ala Gln | Gln Ser Phe Ile | His Arg     |     |  |     |
| 660                 | 665                 | 670             |             |     |  |     |
| Asp Leu Lys Pro Ser | Asn Ile Leu Leu Gly | Asp Asp Met Arg | Ala Lys     |     |  |     |
| 675                 | 680                 | 685             |             |     |  |     |
| Val Ala Asp Phe Gly | Leu Val Lys Asn Ala | Pro Asp Gly Lys | Tyr Ser     |     |  |     |
| 690                 | 695                 | 700             |             |     |  |     |
| Val Glu Thr Arg Leu | Ala Gly Thr Phe Gly | Tyr Leu Ala Pro | Glu Tyr     |     |  |     |
| 705                 | 710                 | 715             | 720         |     |  |     |
| Ala Ala Thr Gly Arg | Val Thr Thr Lys Val | Asp Val Tyr Ala | Phe Gly     |     |  |     |
| 725                 | 730                 | 735             |             |     |  |     |
| Val Val Leu Met Glu | Leu Ile Thr Gly Arg | Lys Ala Leu Asp | Asp Thr     |     |  |     |
| 740                 | 745                 | 750             |             |     |  |     |
| Val Pro Asp Glu Arg | Ser His Leu Val Thr | Trp Phe Arg Arg | Val Leu     |     |  |     |
| 755                 | 760                 | 765             |             |     |  |     |
| Ile Asn Lys Glu Asn | Ile Pro Lys Ala Ile | Asp Gln Ile Leu | Asn Pro     |     |  |     |
| 770                 | 775                 | 780             |             |     |  |     |
| Asp Glu Glu Thr Met | Gly Ser Ile Tyr Thr | Val Ala Glu Leu | Ala Gly     |     |  |     |
| 785                 | 790                 | 795             | 800         |     |  |     |
| His Cys Thr Ala Arg | Glu Pro Tyr Gln Arg | Pro Asp Met Gly | His Ala     |     |  |     |
| 805                 | 810                 | 815             |             |     |  |     |
| Val Asn Val Leu Val | Pro Leu Val Glu Gln | Trp Lys Pro Thr | Ser His     |     |  |     |
| 820                 | 825                 | 830             |             |     |  |     |
| Asp Glu Glu Glu Glu | Asp Gly Ser Gly Gly | Asp Leu His Met | Ser Leu     |     |  |     |
| 835                 | 840                 | 845             |             |     |  |     |
| Pro Gln Ala Leu Arg | Arg Trp Gln Ala Asn | Glu Gly Thr Ser | Ser Ile     |     |  |     |
| 850                 | 855                 | 860             |             |     |  |     |

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys  
 865 870 875 880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg  
 885 890

<210> 1118

<211> 894

<212> PRT

<213> Glycine max

<223> Seq ID: rhg4\_Jack\_amplicon

<400> 1118

Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser  
 1 5 10 15

Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser  
 20 25 30

Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln Ser Leu Thr Gly Thr  
 35 40 45

Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu  
 50 55 60

Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser  
 65 70 75 80

Phe Leu Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Ser  
 85 90 95

Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly  
 100 105 110

Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser  
 115 120 125

Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly  
 130 135 140

Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg  
 145 150 155 160

Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala  
 165 170 175

Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu  
 180 185 190

Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser  
 195 200 205

Trp Leu Asn Lys Asn Gln Phe Thr Gly Ser Ile Pro Asp Leu Ser Gln  
 210 215 220

Cys Thr Ala Leu Ser Asp Leu Gln Leu Arg Asp Asn Gln Leu Thr Gly  
 225 230 235 240  
 Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser Leu Lys Lys Val Ser  
 245 250 255  
 Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro Val Phe Gly Lys Gly  
 260 265 270  
 Val Asn Val Thr Leu Asp Gly Ile Asn Ser Phe Cys Leu Asp Thr Pro  
 275 280 285  
 Gly Asn Cys Asp Pro Arg Val Met Val Leu Leu Gln Ile Ala Glu Ala  
 290 295 300  
 Phe Gly Tyr Pro Ile Arg Leu Ala Glu Ser Trp Lys Gly Asn Asp Pro  
 305 310 315 320  
 Cys Asp Gly Trp Asn Tyr Val Val Cys Ala Ala Gly Lys Ile Ile Thr  
 325 330 335  
 Val Asn Phe Glu Lys Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe  
 340 345 350  
 Ala Asn Leu Thr Asp Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu  
 355 360 365  
 Ile Gly Ser Ile Pro Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr  
 370 375 380  
 Leu Asp Val Ser Asp Asn Asn Leu Ser Gly Leu Val Pro Lys Phe Pro  
 385 390 395 400  
 Pro Lys Val Lys Leu Val Thr Ala Gly Asn Ala Leu Leu Gly Lys Pro  
 405 410 415  
 Leu Ser Pro Gly Gly Gly Pro Ser Gly Thr Thr Pro Ser Gly Ser Ser  
 420 425 430  
 Thr Gly Gly Ser Gly Gly Glu Ser Ser Lys Gly Asn Ser Ser Val Ser  
 435 440 445  
 Pro Gly Trp Ile Ala Gly Ile Val Val Ile Val Leu Phe Phe Ile Ala  
 450 455 460  
 Val Val Leu Phe Val Ser Trp Lys Cys Phe Val Asn Lys Leu Gln Gly  
 465 470 475 480  
 Lys Phe Ser Arg Val Lys Gly His Glu Asn Gly Lys Gly Gly Phe Lys  
 485 490 495  
 Leu Asp Ala Val His Val Ser Asn Gly Tyr Gly Gly Val Pro Val Glu  
 500 505 510  
 Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp  
 515 520 525

Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe  
 530 535 540

Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys  
 545 550 555 560

Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser  
 565 570 575

Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala  
 580 585 590

Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr  
 595 600 605

Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln  
 610 615 620

Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala  
 625 630 635 640

Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg  
 645 650 655

Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg  
 660 665 670

Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys  
 675 680 685

Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser  
 690 695 700

Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr  
 705 710 715 720

Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly  
 725 730 735

Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr  
 740 745 750

Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu  
 755 760 765

Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro  
 770 775 780

Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly  
 785 790 795 800

His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala  
 805 810 815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His  
 820 825 830

Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu

|   |     |         |
|---|-----|---------|
| 835   | 840 | 845     |
| Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile |     |         |
| 850   | 855 | 860     |
| Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys |     |         |
| 865   | 870 | 875 880 |
| Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg         |     |         |
| 885   | 890 |         |
| <210> 1119  |     |         |
| <211> 894   |     |         |
| <212> PRT   |     |         |
| <213> Glycine max   |     |         |
| <223> Seq ID: rhg4_peking_amplicon                              |     |         |
| <400> 1119  |     |         |
| Met Ser Asn Phe Leu Lys Ser Leu Thr Pro Pro Pro Ser Gly Trp Ser |     |         |
| 1   | 5   | 10 15   |
| Glu Thr Thr Pro Phe Cys Gln Trp Lys Gly Ile Gln Cys Asp Ser Ser |     |         |
|   | 20  | 25 30   |
| Ser His Val Thr Ser Ile Ser Leu Ala Ser Gln Ser Leu Thr Gly Thr |     |         |
|   | 35  | 40 45   |
| Leu Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu |     |         |
|   | 50  | 55 60   |
| Gln Asp Asn Ser Leu Thr Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser |     |         |
| 65  | 70  | 75 80   |
| Phe Leu Gln Thr Val Tyr Phe Asn Arg Asn Asn Phe Ser Ser Val Ser |     |         |
|   | 85  | 90 95   |
| Pro Thr Ala Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly |     |         |
|   | 100 | 105 110 |
| Ser Asn Pro Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser |     |         |
|   | 115 | 120 125 |
| Ser Ser Asn Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly |     |         |
|   | 130 | 135 140 |
| Pro Leu Pro Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg |     |         |
| 145   | 150 | 155 160 |
| Leu Ser Tyr Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala |     |         |
|   | 165 | 170 175 |
| Ala Asn Asn Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu |     |         |
|   | 180 | 185 190 |
| Ser Gly Thr Leu Leu Val Leu Ser Asn Met Ser Ala Leu Asn Gln Ser |     |         |

| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Leu | Asn | Lys | Asn | Gln | Phe | Thr | Gly | Ser | Ile | Pro | Asp | Leu | Ser | Gln |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Thr | Ala | Leu | Ser | Asp | Leu | Gln | Leu | Arg | Asp | Asn | Gln | Leu | Thr | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Val | Pro | Ala | Ser | Leu | Thr | Ser | Leu | Pro | Ser | Leu | Lys | Lys | Val | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Asp | Asn | Asn | Glu | Leu | Gln | Gly | Pro | Val | Pro | Val | Phe | Gly | Lys | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Asn | Val | Thr | Leu | Asp | Gly | Ile | Asn | Ser | Phe | Cys | Leu | Asp | Thr | Pro |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Asn | Cys | Asp | Pro | Arg | Val | Met | Val | Leu | Leu | Gln | Ile | Ala | Glu | Ala |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Gly | Tyr | Pro | Ile | Arg | Leu | Ala | Glu | Ser | Trp | Lys | Gly | Asn | Asp | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Cys | Asp | Gly | Trp | Asn | Tyr | Val | Val | Cys | Ala | Ala | Gly | Lys | Ile | Ile | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Asn | Phe | Glu | Lys | Gln | Gly | Leu | Gln | Gly | Thr | Ile | Ser | Pro | Ala | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Asn | Leu | Thr | Asp | Leu | Arg | Thr | Leu | Phe | Leu | Asn | Gly | Asn | Asn | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Gly | Ser | Ile | Pro | Asp | Ser | Leu | Ile | Thr | Leu | Pro | Gln | Leu | Gln | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Asp | Val | Ser | Asp | Asn | Asn | Leu | Ser | Gly | Leu | Val | Pro | Lys | Phe | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Lys | Val | Lys | Leu | Val | Thr | Ala | Gly | Asn | Ala | Leu | Leu | Gly | Lys | Pro |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Ser | Pro | Gly | Gly | Gly | Pro | Ser | Gly | Thr | Thr | Pro | Ser | Gly | Ser | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Gly | Gly | Ser | Gly | Gly | Glu | Ser | Ser | Lys | Gly | Asn | Ser | Ser | Val | Ser |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Pro | Gly | Trp | Ile | Ala | Gly | Ile | Val | Val | Ile | Val | Leu | Phe | Phe | Ile | Ala |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Val | Leu | Phe | Val | Ser | Trp | Lys | Cys | Phe | Val | Asn | Lys | Leu | Gln | Gly |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Lys | Phe | Ser | Arg | Val | Lys | Gly | His | Glu | Asn | Gly | Lys | Gly | Gly | Phe | Lys |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Leu | Asp | Ala | Val | His | Val | Ser | Asn | Gly | Tyr | Gly | Gly | Val | Pro | Val | Glu |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |



Leu Gln Ser Gln Ser Ser Gly Asp Arg Ser Asp Leu His Ala Leu Asp  
 515 520 525  
 Gly Pro Thr Phe Ser Ile Gln Val Leu Arg Gln Val Thr Asn Asn Phe  
 530 535 540  
 Ser Glu Glu Asn Ile Leu Gly Arg Gly Gly Phe Gly Val Val Tyr Lys  
 545 550 555 560  
 Gly Val Leu His Asp Gly Thr Lys Ile Ala Val Lys Arg Met Glu Ser  
 565 570 575  
 Val Ala Met Gly Asn Lys Gly Gln Lys Glu Phe Glu Ala Glu Ile Ala  
 580 585 590  
 Leu Leu Ser Lys Val Arg His Arg His Leu Val Ala Leu Leu Gly Tyr  
 595 600 605  
 Cys Ile Asn Gly Asn Glu Arg Leu Leu Val Tyr Glu Tyr Met Pro Gln  
 610 615 620  
 Gly Thr Leu Thr Gln His Leu Phe Glu Trp Gln Glu His Gly Tyr Ala  
 625 630 635 640  
 Pro Leu Thr Trp Lys Gln Arg Val Val Ile Ala Leu Asp Val Ala Arg  
 645 650 655  
 Gly Val Glu Tyr Leu His Ser Leu Ala Gln Gln Ser Phe Ile His Arg  
 660 665 670  
 Asp Leu Lys Pro Ser Asn Ile Leu Leu Gly Asp Asp Met Arg Ala Lys  
 675 680 685  
 Val Ala Asp Phe Gly Leu Val Lys Asn Ala Pro Asp Gly Lys Tyr Ser  
 690 695 700  
 Val Glu Thr Arg Leu Ala Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr  
 705 710 715 720  
 Ala Ala Thr Gly Arg Val Thr Thr Lys Val Asp Val Tyr Ala Phe Gly  
 725 730 735  
 Val Val Leu Met Glu Leu Ile Thr Gly Arg Lys Ala Leu Asp Asp Thr  
 740 745 750  
 Val Pro Asp Glu Arg Ser His Leu Val Thr Trp Phe Arg Arg Val Leu  
 755 760 765  
 Ile Asn Lys Glu Asn Ile Pro Lys Ala Ile Asp Gln Ile Leu Asn Pro  
 770 775 780  
 Asp Glu Glu Thr Met Gly Ser Ile Tyr Thr Val Ala Glu Leu Ala Gly  
 785 790 795 800  
 His Cys Thr Ala Arg Glu Pro Tyr Gln Arg Pro Asp Met Gly His Ala  
 805 810 815

Val Asn Val Leu Val Pro Leu Val Glu Gln Trp Lys Pro Thr Ser His  
                     820                    825                    830

Asp Glu Glu Glu Glu Asp Gly Ser Gly Gly Asp Leu His Met Ser Leu  
                     835                    840                    845

Pro Gln Ala Leu Arg Arg Trp Gln Ala Asn Glu Gly Thr Ser Ser Ile  
                     850                    855                    860

Phe Asn Asp Ile Ser Ile Ser Gln Thr Gln Ser Ser Ile Ser Ser Lys  
 865                    870                    875                    880

Pro Ala Gly Phe Ala Asp Ser Phe Asp Ser Met Asp Cys Arg  
                     885                    890

<210> 1120

<211> 23

<212> PRT

<213> Artificial

<223> Seq ID: consensusLRR

<400> 1120

Leu Phe Ser Asn Leu Pro Asn Leu Glu Glu Leu Asp Leu Ser Asn Asn  
 1                    5                    10                    15

Leu Thr Ser Leu Pro Pro Gly  
                     20

<210> 1121

<211> 289

<212> PRT

<213> Artifical

<223> Seq ID: rhg1LRR

<400> 1121

Thr Leu Gly Leu Leu Pro Gly Leu Arg Lys Leu Ser Leu His Asp Asn  
 1                    5                    10                    15

Gln Ile Gly Gly Ser Ile Pro Ser Ser Leu Gly Phe Cys Pro Asn Leu  
                     20                    25                    30

Arg Gly Val Gln Leu Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu  
                     35                    40                    45

Leu Ala Asn Ser Thr Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu  
 50 55 60  
 Leu Thr Gly Ala Ile Pro Tyr Ser Leu Thr His Ser Phe Lys Leu Tyr  
 65 70 75 80  
 Trp Leu Asn Leu Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser  
 85 90 95  
 Trp Gly Gly Asn Ser Lys Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn  
 100 105 110  
 Asn Leu Ser Gly Ser Leu Pro Asn Ser Leu Gly Ser Leu Arg Arg Leu  
 115 120 125  
 Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala  
 130 135 140  
 Ser Ile Gly Thr Leu Ser Glu Leu Asn Glu Leu Ser Leu Ser His Asn  
 145 150 155 160  
 Lys Phe Ser Gly Ala Ile Pro Asn Glu Thr Leu Ser Asn Leu Ser Arg  
 165 170 175  
 Leu Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro  
 180 185 190  
 Ala Ser Leu Gly Arg Leu Arg Ser Leu Thr Leu Leu Asn Ala Glu Asn  
 195 200 205  
 Asn Leu Leu Asp Asn Gln Ile Pro Gln Ser Ile Ala Asn Ile Ser Asn  
 210 215 220  
 Leu Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile Pro  
 225 230 235 240  
 Ser Ser Phe Asp Ser Gln Arg Ser Leu Arg Gln Leu Asp Leu Ser Leu  
 245 250 255  
 Asn Asn Phe Ser Gly Glu Ile Pro Val Leu Leu Ala Lys Lys Phe Asn  
 260 265 270  
 Ser Leu Asn Leu Phe Asn Val Ser Asn Ser Leu Ser Gly Ser Val Pro  
 275 280 285

Pro

&lt;210&gt; 1122

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;223&gt; Seq ID: Rhg4LRR

&lt;400&gt; 1122

His Val Thr Ser Ile Ser Leu Ala Ser His Ser Leu Thr Gly Thr Leu  
1 5 10 15

Pro Ser Asp Leu Asn Ser Leu Ser Gln Leu Arg Thr Leu Ser Leu Gln  
20 25 30

Asp Asn Ser Leu Gly Thr Leu Pro Ser Leu Ser Asn Leu Ser Phe Leu  
35 40 45

Gln Thr Val Tyr Leu Asn Arg Asn Asn Phe Ser Ser Val Pro Thr Ala  
50 55 60

Phe Ala Ser Leu Thr Ser Leu Gln Thr Leu Ser Leu Gly Ser Asn Pro  
65 70 75 80

Ala Leu Gln Pro Trp Ser Phe Pro Thr Asp Leu Thr Ser Ser Ser Asn  
85 90 95

Leu Ile Asp Leu Asp Leu Ala Thr Val Ser Leu Thr Gly Pro Leu Pro  
100 105 110

Asp Ile Phe Asp Lys Phe Pro Ser Leu Gln His Leu Arg Leu Ser Tyr  
115 120 125

Asn Asn Leu Thr Gly Asn Leu Pro Ser Ser Phe Ser Ala Ala Asn Asn  
130 135 140

Leu Glu Thr Leu Trp Leu Asn Asn Gln Ala Ala Gly Leu Ser Gly Thr  
145 150 155 160

Leu Leu Leu Ser Asn Met Ser Ala Leu Ser Asp Leu Gln Leu Arg Asp  
165 170 175

Asn Gln Leu Thr Gly Val Val Pro Ala Ser Leu Thr Ser Leu Pro Ser  
180 185 190

Leu Lys Lys Val Ser Leu Asp Asn Asn Glu Leu Gln Gly Pro Val Pro  
195 200 205

Val Phe Gly Lys Gly Val Asn Lys Ile Ile Thr Val Asn Phe Glu Lys  
210 215 220

Gln Gly Leu Gln Gly Thr Ile Ser Pro Ala Phe Ala Asn Leu Thr Asp  
225 230 235 240

Leu Arg Thr Leu Phe Leu Asn Gly Asn Asn Leu Ile Gly Ser Ile Pro  
245 250 255

Asp Ser Leu Ile Thr Leu Pro Gln Leu Gln Thr Leu Asp Val Ser Asp  
260 265 270

Asn Asn Leu Ser Gly Leu Val Pro Lys  
275 280

<210> 1123

<211> 27

<212> DNA

<213> Glycine max

<223> Seq ID: 240017\_region\_G3\_forward\_1\_b

<400> 1123

gttgatatgga tggtaaaaat tcaaaac

27